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<110> Bristol-Myers Squibb Company

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<151> 2000-12-04

<150> 60/263,678

<151> 2001-01-23

<150> 60/273,037

<151> 2001-03-02

<160> 1579

<170> PatentIn version 3.0

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 Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp
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 Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn
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Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val
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Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met
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Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser
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His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu
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Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe
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145 150 155																
gtg ctc atc tgg gtt gtg ggg ggc ctc ttg agc atc ccc aca ttc ctg Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu																528
160 165 170																
ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile																576
175 180 185 190																
ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta Leu Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu																624
195 200 205																
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210 215 220																
tac cac atc ctg gcc tcc ctg cga acg cgg gag gag gtc agc agg aca Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr																720
225 230 235																
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240 245 250																
ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc																816

Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala
 255 260 265 270

 ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg 864
 Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp
 275 280 285

 gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc 912
 Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe
 290 295 300

 act aac agc tcc ctg aat cca gta att tat gtc ttt gtg ggc cgg ctc 960
 Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu
 305 310 315

 ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt 1008
 Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser
 320 325 330

 ctt gct cca ata tct tca tcc cat agg aaa gaa atc ttc caa ctt ttc 1056
 Leu Ala Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe
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 Trp Arg Asn

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 35 40 45

 Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
 50 55 60

 Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
 65 70 75 80

 Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
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Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
 130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
 195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
 210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
 225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
 245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
 260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
 275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
 290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
 305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
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Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
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 Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn
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 Gln Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro
 15 20 25 30

gaa gcc tgg gac ctg ctg cac aga gtg ctg ccg aca ttt atc atc tcc 144
 Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser
 35 40 45

atc tgt ttc ttc ggc ctc cta ggg aac ctt ttt gtc ctg ttg gtc ttc 192
 Ile Cys Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe
 50 55 60

ctc ctg ccc cgg cgg caa ctg aac gtg gca gaa atc tac ctg gcc aac 240
 Leu Leu Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn
 65 70 75

ctg gca gcc tct gat ctg gtg ttt gtc ttg ggc ttg ccc ttc tgg gca 288
 Leu Ala Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala
 80 85 90

gag aat atc tgg aac cag ttt aac tgg cct ttc gga gcc ctc ctc tgc 336
 Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys
 95 100 105 110

cgt gtc atc aac ggg gtc atc aag gcc aat ttg ttc atc agc atc ttc 384
 Arg Val Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe
 115 120 125

ctg gtg gtg gcc atc agc cag gac cgc tac cgc gtg ctg gtg cac cct 432
 Leu Val Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro

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130	135	140	
atg gcc agc gga agg cag cag cgg cgg agg cag gcc cgg gtc acc tgc			480
Met Ala Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys			
145	150	155	
gtg ctc atc tgg gtt gtg ggg ggc ctc ttg agc atc ccc aca ttc ctg			528
Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu			
160	165	170	
ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc			576
Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile			
175	180	185	190
ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta			624
Leu Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu			
	195	200	205
aat att ctg ggt ttc ctc cta cca ctg gct gcg atc gtc ttc ttc aac			672
Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn			
	210	215	220
tac cac atc ctg gcc tcc ctg cga acg cgg gag gag gtc agc agg aca			720
Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr			
	225	230	235
aga gtg cgg ggg ccg aag gat agc aag acc aca gcg ctg atc ctc acg			768
Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr			
	240	245	250
ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc			816
Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala			
255	260	265	270
ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg			864
Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp			
	275	280	285
gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc			912
Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe			
	290	295	300
act aac agc tcc ctg aat cca gta att tat gtc ttt gtg ggc cag ctc			960
Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Gln Leu			
	305	310	315
ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt			1008
Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser			
	320	325	330
ctt gct cca ata tct tca tcc cat agg aaa gaa atc ttc caa ctt ttc			1056
Leu Ala Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe			
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tggt cgg aat taaaacagca ttgaacc			1082
Trp Arg Asn			

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<400> 8

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
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Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
 130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
 195 200 205
 Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
 210 215 220
 Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
 225 230 235 240
 Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
 245 250 255
 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
 260 265 270
 Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
 275 280 285
 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
 290 295 300
 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Gln Leu Phe Arg
 305 310 315 320
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Asn

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cag agc cag ctc ttc cct caa aat gct acg gcc tgt gac aat gct cca Gln Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro 15 20 25 30	96
gaa gcc tgg gac ctg ctg cac aga gtg ctg cca aca ttt atc atc tcc Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser 35 40 45	144
atc tgt ttc ttc ggc ctc cta ggg aac ctt ttt gtc ctg ttg gtc ttc Ile Cys Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe 50 55 60	192
ctc ctg ccc cgg cgg caa ctg aac gtg gca gaa atc tac ctg gcc aac Leu Leu Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn 65 70 75	240
ctg gca gcc tct gat ctg gtg ttt gtc ttg ggc ttg ccc ttc tgg gca Leu Ala Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala 80 85 90	288
gag aat atc tgg aac cag ttt aac tgg cct ttc gga gcc ctc ctc tgc Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys 95 100 105 110	336
cgt gtc atc aac ggg gtc atc aag gcc aat ttg ttc atc agc atc ttc Arg Val Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe 115 120 125	384
ctg gtg gtg gcc atc agc cag gac cgc tac cgc gtg ctg gtg cac cct Leu Val Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro 130 135 140	432
atg gcc agc gga agg cag cag cgg cgg agg cag gcc cgg gtc acc tgc Met Ala Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys 145 150 155	480
gtg ctc atc tgg gtt gtg ggg ggc ctc ttg agc atc ccc aca ttc ctg Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu 160 165 170	528
ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile 175 180 185 190	576
ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta Leu Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu 195 200 205	624
aat att ctg ggt ttc ctc cta cca ctg gct gcg atc gtc ttc ttc aac Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn 210 215 220	672
tac cac atc ctg gcc tcc ctg cga acg cgg gag gag gtc agc agg aca Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr 225 230 235	720

aga gtg cgg ggg ccg aag gat agc aag acc aca gcg ctg atc ctc acg 768
 Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr
 240 245 250

ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc 816
 Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala
 255 260 265 270

ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg 864
 Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp
 275 280 285

gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc 912
 Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe
 290 295 300

act aac agc tcc ctg aat cca gta att tat gtc ttt gtg ggc cgg ctc 960
 Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu
 305 310 315

ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt 1008
 Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser
 320 325 330

ctt gct cca ata tct tca tcc cat agg aaa gaa atc ttc caa ctt ttc 1056
 Leu Ala Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe
 335 340 345 350

tgg cgg aat taaaacagca ttgaacc 1082
 Trp Arg Asn

<210> 10
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Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
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Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala

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Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
325 330 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
340 345 350

Asn

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Met Phe Ser Pro Trp Lys Ile Ser Met Phe Leu Ser Val Arg Glu Asp
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tcc gtg ccc acc acg gcc tct ttc agc gcc gac atg ctc aat gtc acc 96
Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr
20 25 30
ttg caa ggg ccc act ctt aac ggg acc ttt gcc cag agc aaa tgc ccc 144
Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro
35 40 45
caa gtg gag tgg ctg ggc tgg ctc aac acc atc cag ccc ccc ttc ctc 192
Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
50 55 60
tgg gtg ctg ttc gtg ctg gcc acc cta gag aac atc ttt gtc ctc agc 240
Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
65 70 75 80
gtc ttc tgc ctg cac aag agc agc tgc acg gtg gca gag atc tac ctg 288
Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
85 90 95
ggg aac ctg gcc gca gca gac ctg atc ctg gcc tgc ggg ctg ccc ttc 336
Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
100 105 110
tgg gcc atc acc atc tcc aac aac ttc gac tgg ctc ttt ggg gag acg 384

Trp	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Asp	Trp	Leu	Phe	Gly	Glu	Thr		
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Leu	Cys	Arg	Val	Val	Asn	Ala	Ile	Ile	Ser	Met	Asn	Leu	Tyr	Ser	Ser		
	130					135					140						
atc	tgt	ttc	ctg	atg	ctg	gtg	agc	atc	gac	cgc	tac	ctg	gcc	ctg	gtg		480
Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Leu	Val		
145					150				155						160		
aaa	acc	atg	tcc	atg	ggc	cgg	atg	cgc	ggc	gtg	cgc	tgg	gcc	aag	ctc		528
Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	Val	Arg	Trp	Ala	Lys	Leu		
				165					170					175			
tac	agc	ttg	gtg	atc	tgg	ggg	tgt	acg	ctg	ctc	ctg	agc	tca	ccc	atg		576
Tyr	Ser	Leu	Val	Ile	Trp	Gly	Cys	Thr	Leu	Leu	Leu	Ser	Ser	Pro	Met		
			180				185						190				
ctg	gtg	ttc	cgg	acc	atg	aag	gag	tac	agc	gat	gag	ggc	cac	aac	gtc		624
Leu	Val	Phe	Arg	Thr	Met	Lys	Glu	Tyr	Ser	Asp	Glu	Gly	His	Asn	Val		
		195					200					205					
acc	gct	tgt	gtc	atc	agc	tac	cca	tcc	ctc	atc	tgg	gaa	gtg	ttc	acc		672
Thr	Ala	Cys	Val	Ile	Ser	Tyr	Pro	Ser	Leu	Ile	Trp	Glu	Val	Phe	Thr		
	210					215					220						
aac	atg	ctc	ctg	aat	gtc	gtg	ggc	ttc	ctg	ctg	ccc	ctg	agt	gtc	atc		720
Asn	Met	Leu	Leu	Asn	Val	Val	Gly	Phe	Leu	Leu	Pro	Leu	Ser	Val	Ile		
225					230				235					240			
acc	ttc	tgc	acg	atg	cag	atc	atg	cag	gtg	ctg	cgg	aac	aac	gag	atg		768
Thr	Phe	Cys	Thr	Met	Gln	Ile	Met	Gln	Val	Leu	Arg	Asn	Asn	Glu	Met		
				245				250						255			
cag	aag	ttc	aag	gag	atc	cag	acg	gag	agg	agg	gcc	acg	gtg	cta	gtc		816
Gln	Lys	Phe	Lys	Glu	Ile	Gln	Thr	Glu	Arg	Arg	Ala	Thr	Val	Leu	Val		
			260				265						270				
ctg	gtt	gtg	ctg	ctg	cta	ttc	atc	atc	tgc	tgg	ctg	ccc	ttc	cag	atc		864
Leu	Val	Val	Leu	Leu	Leu	Phe	Ile	Ile	Cys	Trp	Leu	Pro	Phe	Gln	Ile		
		275					280					285					
agc	acc	ttc	ctg	gat	acg	ctg	cat	cgc	ctc	ggc	atc	ctc	tcc	agc	tgc		912
Ser	Thr	Phe	Leu	Asp	Thr	Leu	His	Arg	Leu	Gly	Ile	Leu	Ser	Ser	Cys		
	290					295				300							
cag	gac	gag	cgc	atc	atc	gat	gta	atc	aca	cag	atc	gcc	tcc	ttc	atg		960
Gln	Asp	Glu	Arg	Ile	Ile	Asp	Val	Ile	Thr	Gln	Ile	Ala	Ser	Phe	Met		
305					310				315						320		
gcc	tac	agc	aac	agc	tgc	ctc	aac	cca	ctg	gtg	tac	gtg	atc	gtg	ggc		1008
Ala	Tyr	Ser	Asn	Ser	Cys	Leu	Asn	Pro	Leu	Val	Tyr	Val	Ile	Val	Gly		
				325				330					335				
aag	cgc	ttc	cga	aag	aag	tct	tgg	gag	gtg	tac	cag	gga	gtg	tgc	cag		1056
Lys	Arg	Phe	Arg	Lys	Lys	Ser	Trp	Glu	Val	Tyr	Gln	Gly	Val	Cys	Gln		

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aaa ggg ggc tgc agg tca gaa ccc att cag atg gag aac tcc atg ggc			1104
Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly			
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aca ctg cgg acc tcc atc tcc gtg gaa cgc cag att cac aaa ctg cag			1152
Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln			
370	375	380	
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Asp Trp Ala Gly Ser Arg Gln			
385	390		
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tgccctgccc aattttgcag ggagcatggc tgtgaggatg ggggtgaactc acgcacagcc			1383
aaggactcca aaatcacaac agcattactg ttcttatttg ctgccacacc tgagccagcc			1443
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gggactgttc ctgtctcagc aaccaaggga ttgttcctgt caatcaatgg tttattggaa			2523


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ggtggccag tatgagccct agaagagtgt gaaaaggaat ggcaatggtg ttcaccatcg 2583
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gctagaacca agaagggcta gaacctggag gggctagaac ctagagaagc taaaacctga 2763
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Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr
20           25           30

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Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro
 35 40 45

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
 50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
 65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
 115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser
 130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val
 145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu
 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met
 180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val
 195 200 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr
 210 215 220

Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile
 225 230 235 240

Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met
 245 250 255

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Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val
      260                      265                      270

Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile
      275                      280                      285

Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
      290                      295                      300

Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
      305                      310                      315                      320

Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
      325                      330                      335

Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
      340                      345                      350

Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly
      355                      360                      365

Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln
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Asp Trp Ala Gly Ser Arg Gln
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<222> (211)..(1431)

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cagttcagct ttcaaaaaga gtgctgccca taaaaagcct tccaccctcc tgtctgcttt      120
agaaggaccc tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta      180
cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac      234
          Met Asp Asn Val Leu Pro Val Asp
          1                      5

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tca gac ctc tcc cca aac atc tcc act aac acc tcg gaa ccc aat cag	282
Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln	
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ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg	330
Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr	
25 30 35 40	
gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc	378
Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile	
45 50 55	
atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg	426
Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val	
60 65 70	
aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg	474
Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val	
75 80 85	
aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac	522
Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr	
90 95 100	
tgc aag ttc cac aac ttc ttt ccc atc gcc gct gtc ttc gcc agt atc	570
Cys Lys Phe His Asn Phe Phe Pro Ile Ala Ala Val Phe Ala Ser Ile	
105 110 115 120	
tac tcc atg acg gct gtg gcc ttt gat agg tac atg gcc atc ata cat	618
Tyr Ser Met Thr Ala Val Ala Phe Asp Arg Tyr Met Ala Ile Ile His	
125 130 135	
ccc ctc cag ccc cgg ctg tca gcc aca gcc acc aaa gtg gtc atc tgt	666
Pro Leu Gln Pro Arg Leu Ser Ala Thr Ala Thr Lys Val Val Ile Cys	
140 145 150	
gtc atc tgg gtc ctg gct ctc ctg ctg gcc ttc ccc cag ggc tac tac	714
Val Ile Trp Val Leu Ala Leu Leu Leu Ala Phe Pro Gln Gly Tyr Tyr	
155 160 165	
tca acc aca gag acc atg ccc agc aga gtc gtg tgc atg atc gaa tgg	762
Ser Thr Thr Glu Thr Met Pro Ser Arg Val Val Cys Met Ile Glu Trp	
170 175 180	
cca gag cat ccg aac aag att tat gag aaa gtg tac cac atc tgt gtg	810
Pro Glu His Pro Asn Lys Ile Tyr Glu Lys Val Tyr His Ile Cys Val	
185 190 195 200	
act gtg ctg atc tac ttc ctc ccc ctg ctg gtg att ggc tat gca tac	858
Thr Val Leu Ile Tyr Phe Leu Pro Leu Leu Val Ile Gly Tyr Ala Tyr	
205 210 215	
acc gta gtg gga atc aca cta tgg gcc agt gag atc ccc ggg gac tcc	906
Thr Val Val Gly Ile Thr Leu Trp Ala Ser Glu Ile Pro Gly Asp Ser	
220 225 230	
tct gac cgc tac cac gag caa gtc tct gcc aag cgc aag gtg gtc aaa	954

Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys		
		235					240					245					
atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc	1002	
Met	Met	Ile	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Phe		
		250				255					260						
cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag	1050	
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys		
265					270					275					280		
aag	ttt	atc	cag	cag	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc	1098	
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser		
			285						290					295			
tcc	acc	atg	tac	aac	ccc	atc	atc	tac	tgc	tgc	ctc	aat	gac	agg	ttc	1146	
Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe		
			300					305					310				
cgt	ctg	ggc	ttc	aag	cat	gcc	ttc	cgg	tgc	tgc	ccc	ttc	atc	agc	gcc	1194	
Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala		
		315					320					325					
ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc	1242	
Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Lys	Ser	Thr	Arg	Tyr	Leu	Gln	Thr		
	330					335					340						
cag	ggc	agt	gtg	tac	aaa	gtc	agc	cgc	ctg	gag	acc	acc	atc	tcc	aca	1290	
Gln	Gly	Ser	Val	Tyr	Lys	Val	Ser	Arg	Leu	Glu	Thr	Thr	Ile	Ser	Thr		
345					350					355					360		
gtg	gtg	ggg	gcc	cac	gag	gag	gag	cca	gag	gac	ggc	ccc	aag	gcc	aca	1338	
Val	Val	Gly	Ala	His	Glu	Glu	Glu	Pro	Glu	Asp	Gly	Pro	Lys	Ala	Thr		
				365					370					375			
ccc	tgc	tcc	ctg	gac	ctg	acc	tcc	aac	tgc	tct	tca	cga	agt	gac	tcc	1386	
Pro	Ser	Ser	Leu	Asp	Leu	Thr	Ser	Asn	Cys	Ser	Ser	Arg	Ser	Asp	Ser		
			380					385					390				
aag	acc	atg	aca	gag	agc	ttc	agc	ttc	tcc	tcc	aat	gtg	ctc	tcc		1431	
Lys	Thr	Met	Thr	Glu	Ser	Phe	Ser	Phe	Ser	Ser	Asn	Val	Leu	Ser			
		395					400					405					
taggccacag	ggccttttggc	aggtgcagcc	cccactgcct	ttgacctgcc	tcccttcatg											1491	
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taaaataaaa	ggcgggacca	gcttttccctc	aagagcccaa	tgcatcccat	ttctggaagt											1731	
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<400> 14

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Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
 35 40 45

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
 50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
 65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
 85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
 100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
 115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
 130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
 145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
 165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
 180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
 195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
 210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
 225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
 245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
 260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
 275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser
 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
 355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser
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Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser
 385 390 395 400

Phe Ser Ser Asn Val Leu Ser
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<220>
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 <222> (211)..(1431)

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agaaggacct tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta      180

cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac      234
                Met Asp Asn Val Leu Pro Val Asp
                1                    5

tca gac ctc tcc cca aac atc tcc act aac acc tcg gaa ccc aat cag      282
Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln
    10                    15                    20

ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg      330
Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr
    25                    30                    35                    40

gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc      378
Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile
                45                    50                    55

atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg      426
Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val
                60                    65                    70

aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg      474
Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val
                75                    80                    85

aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac      522
Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr
    90                    95                    100

tgc aag ttc cac aac ttc ttc ccc atc gcc gct gtc ttc gcc agt atc      570
Cys Lys Phe His Asn Phe Phe Pro Ile Ala Ala Val Phe Ala Ser Ile
    105                    110                    115                    120

tac tcc atg acg gct gtg gcc ttt gat agg tac atg gcc atc ata cat      618
Tyr Ser Met Thr Ala Val Ala Phe Asp Arg Tyr Met Ala Ile Ile His
                125                    130                    135

ccc ctc cag ccc cgg ctg tca gcc aca gcc acc aaa gtg gtc atc tgt      666
Pro Leu Gln Pro Arg Leu Ser Ala Thr Ala Thr Lys Val Val Ile Cys
                140                    145                    150

gtc atc tgg gtc ctg gct ctc ctg ctg gcc ttc ccc cag ggc tac tac      714
Val Ile Trp Val Leu Ala Leu Leu Leu Ala Phe Pro Gln Gly Tyr Tyr
                155                    160                    165

tca acc aca gag acc atg ccc agc aga gtc gtg tgc atg atc gaa tgg      762

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Ser	Thr	Thr	Glu	Thr	Met	Pro	Ser	Arg	Val	Val	Cys	Met	Ile	Glu	Trp		
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Pro	Glu	His	Pro	Asn	Lys	Ile	Tyr	Glu	Lys	Val	Tyr	His	Ile	Cys	Val		
185					190					195					200		
act	gtg	ctg	atc	tac	ttc	ctc	ccc	ctg	ctg	gtg	att	ggc	tat	gca	tac	858	
Thr	Val	Leu	Ile	Tyr	Phe	Leu	Pro	Leu	Leu	Val	Ile	Gly	Tyr	Ala	Tyr		
				205						210				215			
acc	gta	gtg	gga	atc	aca	cta	tgg	gcc	agt	gag	atc	ccc	ggg	gac	tcc	906	
Thr	Val	Val	Gly	Ile	Thr	Leu	Trp	Ala	Ser	Glu	Ile	Pro	Gly	Asp	Ser		
			220					225					230				
tct	gac	cgc	tac	cac	gag	caa	gtc	tct	gcc	aag	cgc	aag	gtg	gtc	aaa	954	
Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys		
		235					240					245					
atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc	1002	
Met	Met	Ile	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Phe		
						255						260					
cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag	1050	
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys		
					270					275					280		
aag	ttt	atc	cag	cag	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc	1098	
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser		
				285					290					295			
tcc	acc	atg	tac	aac	ccc	atc	atc	tac	tgc	tgc	ctc	aat	gac	agg	ttc	1146	
Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe		
			300					305					310				
cgt	ctg	ggc	ttc	aag	cat	gcc	ttc	cgg	tgc	tgc	ccc	ttc	atc	agc	gcc	1194	
Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala		
			315				320					325					
ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc	1242	
Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Lys	Ser	Thr	Arg	Tyr	Leu	Gln	Thr		
			330			335					340						
cag	ggc	agt	gtg	tac	aaa	gtc	agc	cgc	ctg	gag	acc	acc	atc	tcc	aca	1290	
Gln	Gly	Ser	Val	Tyr	Lys	Val	Ser	Arg	Leu	Glu	Thr	Thr	Ile	Ser	Thr		
					350					355					360		
gtg	gtg	ggg	gcc	cac	gag	gag	gag	cca	gag	gac	ggc	ccc	aag	gcc	aca	1338	
Val	Val	Gly	Ala	His	Glu	Glu	Glu	Pro	Glu	Asp	Gly	Pro	Lys	Ala	Thr		
				365					370					375			
ccc	tcg	tcc	ctg	gac	ctg	acc	tcc	aac	tgc	tct	tca	cga	agt	gac	tcc	1386	
Pro	Ser	Ser	Leu	Asp	Leu	Thr	Ser	Asn	Cys	Ser	Ser	Arg	Ser	Asp	Ser		
			380					385					390				
aag	acc	atg	aca	gag	agc	ttc	agc	ttc	tcc	tcc	aat	gtg	ctc	tcc		1431	
Lys	Thr	Met	Thr	Glu	Ser	Phe	Ser	Phe	Ser	Ser	Asn	Val	Leu	Ser			

395	400	405	
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gggtcagtat	gggttaggga	aaacattcca	tccttgagtc aaaaaatctc aattcttccc 1611
tatctttgcc	accctcatgc	tgtgtgactc	aaaccaaadc actgaacttt gctgagcctg 1671
taaaataaaa	ggcgcgacca	gcttttcctc	aagagcccaa tgcattccat ttctggaagt 1731
gactttggct	gcatgagagt	gctcatttca	ggatg 1766

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			20					25					30			

Val	Leu	Trp	Ala	Ala	Ala	Tyr	Thr	Val	Ile	Val	Val	Thr	Ser	Val	Val	
	35						40					45				

Gly	Asn	Val	Val	Val	Met	Trp	Ile	Ile	Leu	Ala	His	Lys	Arg	Met	Arg	
	50					55					60					

Thr	Val	Thr	Asn	Tyr	Phe	Leu	Val	Asn	Leu	Ala	Phe	Ala	Glu	Ala	Ser	
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Met	Ala	Ala	Phe	Asn	Thr	Val	Val	Asn	Phe	Thr	Tyr	Ala	Val	His	Asn	
			85					90						95		

Glu	Trp	Tyr	Tyr	Gly	Leu	Phe	Tyr	Cys	Lys	Phe	His	Asn	Phe	Phe	Pro	
		100						105					110			

Ile	Ala	Ala	Val	Phe	Ala	Ser	Ile	Tyr	Ser	Met	Thr	Ala	Val	Ala	Phe	
	115						120					125				

Asp	Arg	Tyr	Met	Ala	Ile	Ile	His	Pro	Leu	Gln	Pro	Arg	Leu	Ser	Ala	
	130					135					140					

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
 145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
 165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
 180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
 195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
 210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
 225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
 245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
 260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
 275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser
 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
 355 360 365

Cys	Lys	Phe	His	Asn	Phe	Phe	Pro	Ile	Ala	Ala	Val	Phe	Ala	Ser	Ile		
105					110					115					120		
tac	tcc	atg	acg	gct	gtg	gcc	ttt	gat	agg	tac	atg	gcc	atc	ata	cat		618
Tyr	Ser	Met	Thr	Ala	Val	Ala	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Ile	His		
				125					130					135			
ccc	ctc	cag	ccc	cgg	ctg	tca	gcc	aca	gcc	acc	aaa	gtg	gtc	atc	tgt		666
Pro	Leu	Gln	Pro	Arg	Leu	Ser	Ala	Thr	Ala	Thr	Lys	Val	Val	Ile	Cys		
			140					145					150				
gtc	ata	tgg	gtc	ctg	gct	ctc	ctg	ctg	gcc	ttc	ccc	cag	ggc	tac	tac		714
Val	Ile	Trp	Val	Leu	Ala	Leu	Leu	Leu	Ala	Phe	Pro	Gln	Gly	Tyr	Tyr		
		155					160					165					
tca	acc	aca	gag	acc	atg	ccc	agc	aga	gtc	gtg	tgc	atg	atc	gaa	tgg		762
Ser	Thr	Thr	Glu	Thr	Met	Pro	Ser	Arg	Val	Val	Cys	Met	Ile	Glu	Trp		
	170					175					180						
cca	gag	cat	ccg	aac	aag	att	tat	gag	aaa	gtg	tac	cac	atc	tgt	gtg		810
Pro	Glu	His	Pro	Asn	Lys	Ile	Tyr	Glu	Lys	Val	Tyr	His	Ile	Cys	Val		
185				190						195				200			
act	gtg	ctg	atc	tac	ttc	ctc	ccc	ctg	ctg	gtg	att	ggc	tat	gca	tac		858
Thr	Val	Leu	Ile	Tyr	Phe	Leu	Pro	Leu	Leu	Val	Ile	Gly	Tyr	Ala	Tyr		
				205				210						215			
acc	gta	gtg	gga	atc	aca	cta	tgg	gcc	agt	gag	atc	ccc	ggg	gac	tcc		906
Thr	Val	Val	Gly	Ile	Thr	Leu	Trp	Ala	Ser	Glu	Ile	Pro	Gly	Asp	Ser		
			220					225					230				
tct	gac	cgc	tac	cac	gag	caa	gtc	tct	gcc	aag	cgc	aag	gtg	gtc	aaa		954
Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys		
		235					240					245					
atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc		1002
Met	Met	Ile	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Phe		
		250				255					260						
cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag		1050
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys		
265					270					275					280		
aag	ttt	atc	cag	cag	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc		1098
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser		
				285				290						295			
tcc	acc	atg	tac	aac	ccc	atc	atc	tac	tgc	tgc	ctc	aat	gac	agg	ttc		1146
Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe		
			300					305					310				
cgt	ctg	ggc	ttc	aag	cat	gcc	ttc	cgg	tgc	tgc	ccc	ttc	atc	agc	gcc		1194
Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala		
		315					320					325					
ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc		1242
Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Lys	Ser	Thr	Arg	Tyr	Leu	Gln	Thr		

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cag ggc agt gtg tac aaa gtc agc cgc ctg gag acc acc atc tcc aca			1290
Gln Gly Ser Val Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr			
345	350	355	360
gtg gtg ggg gcc cac gag gag gag cca gag gac ggc ccc aag gcc aca			1338
Val Val Gly Ala His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr			
	365	370	375
ccc tcg tcc ctg gac ctg acc tcc aac tgc tct tca cga agt gac tcc			1386
Pro Ser Ser Leu Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser			
	380	385	390
aag acc atg aca gag agc ttc agc ttc tcc tcc aat gtg ctc tcc			1431
Lys Thr Met Thr Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser			
	395	400	405
taggccacag ggcctttggc aggtgcagcc cccactgcct ttgacctgcc tcccttcagt			1491
catggaaatt ccccttcatt ggaaccatca gaaacaccct cacactggga cttgcaaaaa			1551
gggtcagtat gggttagggg aaacattcca tccttgagtc aaaaaatctc aattcttccc			1611
tatctttgcc accctcatgc tgtgtgactc aaaccaaadc actgaacttt gctgagcctg			1671
taaaataaaa ggtcggacca gcttttcctc aagagcccaa tgcattccat ttctggaagt			1731
gactttggct gcatgagagt gctcatttca ggatg			1766
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1	5	10	15
Thr Asn Thr Ser Glu Pro Asn Gln Phe Val Gln Pro Ala Trp Gln Ile			
	20	25	30
Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val			
	35	40	45
Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg			
	50	55	60
Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser			
	65	70	75
			80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser
 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
 355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser
 370 375 380

Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser
 385 390 395 400

Phe Ser Ser Asn Val Leu Ser
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 agaaggaccc tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta 180
 cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234
 Met Asp Asn Val Leu Pro Val Asp
 1 5
 tca gac ctc tcc cca aac atc tcc act aac acc tcg gaa ccc aat cag 282
 Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln
 10 15 20
 ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg 330
 Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr
 25 30 35 40
 gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc 378

Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile	
45 50 55	
atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg	426
Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val	
60 65 70	
aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg	474
Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val	
75 80 85	
aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac	522
Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr	
90 95 100	
tgc aag ttc cac aac ttc ttt ccc atc gcc gct gtc ttc gcc agt atc	570
Cys Lys Phe His Asn Phe Phe Pro Ile Ala Ala Val Phe Ala Ser Ile	
105 110 115 120	
tac tcc atg acg gct gtg gcc ttt gat agg tac atg gcc atc ata cat	618
Tyr Ser Met Thr Ala Val Ala Phe Asp Arg Tyr Met Ala Ile Ile His	
125 130 135	
ccc ctc cag ccc cgg ctg tca gcc aca gcc acc aaa gtg gtc atc tgt	666
Pro Leu Gln Pro Arg Leu Ser Ala Thr Ala Thr Lys Val Val Ile Cys	
140 145 150	
gtc atc tgg gtc ctg gct ctc ctg ctg gcc ttc ccc cag ggc tac tac	714
Val Ile Trp Val Leu Ala Leu Leu Leu Ala Phe Pro Gln Gly Tyr Tyr	
155 160 165	
tca acc aca gag acc atg ccc agc aga gtc gtg tgc atg atc gaa tgg	762
Ser Thr Thr Glu Thr Met Pro Ser Arg Val Val Cys Met Ile Glu Trp	
170 175 180	
cca gag cat ccg aac aag att tat gag aaa gtg tac cac atc tgt gtg	810
Pro Glu His Pro Asn Lys Ile Tyr Glu Lys Val Tyr His Ile Cys Val	
185 190 195 200	
act gtg ctg atc tac ttc ctc ccc ctg ctg gtg att ggc tat gca tac	858
Thr Val Leu Ile Tyr Phe Leu Pro Leu Leu Val Ile Gly Tyr Ala Tyr	
205 210 215	
acc gta gtg gga atc aca cta tgg gcc agt gag atc ccc ggg gac tcc	906
Thr Val Val Gly Ile Thr Leu Trp Ala Ser Glu Ile Pro Gly Asp Ser	
220 225 230	
tct gac cgc tac cac gag caa gtc tct gcc aag cgc aag gtg gtc aaa	954
Ser Asp Arg Tyr His Glu Gln Val Ser Ala Lys Arg Lys Val Val Lys	
235 240 245	
atg atg att gtg gtg gtg tgc acc ttc gcc atc tgc tgg ctg ccc ttc	1002
Met Met Ile Val Val Val Cys Thr Phe Ala Ile Cys Trp Leu Pro Phe	
250 255 260	
cac atc ttc ttc ctc ctg ccc tac atc aac cca gat ctc tac ctg aag	1050
His Ile Phe Phe Leu Leu Pro Tyr Ile Asn Pro Asp Leu Tyr Leu Lys	

265	270	275	280	
aag ttt atc cag cag gtc tac ctg gcc atc atg tgg ctg gcc atg agc				1098
Lys Phe Ile Gln Gln Val Tyr Leu Ala Ile Met Trp Leu Ala Met Ser	285	290	295	
tcc acc atg tac aac ccc atc atc tac tgc tgc ctc aat gac agg ttc				1146
Ser Thr Met Tyr Asn Pro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe	300	305	310	
cgt ctg ggc ttc aag cat gcc ttc cgg tgc tgc ccc ttc atc agc gcc				1194
Arg Leu Gly Phe Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala	315	320	325	
ggc gac tat gag ggg ctg gaa atg aaa tcc acc cgg tat ctc cag acc				1242
Gly Asp Tyr Glu Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr	330	335	340	
cag ggc agt gtg tac aaa gtc agc cgc ctg gag acc acc atc tcc aca				1290
Gln Gly Ser Val Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr	345	350	355	360
gtg gtg ggg gcc cac gag gag gag cca gag gac ggc ccc aag gcc aca				1338
Val Val Gly Ala His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr	365	370	375	
ccc tca tcc ctg gac ctg acc tcc aac tgc tct tca cga agt gac tcc				1386
Pro Ser Ser Leu Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser	380	385	390	
aag acc atg aca gag agc ttc agc ttc tcc tcc aat gtg ctc tcc				1431
Lys Thr Met Thr Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser	395	400	405	
taggccacag ggcctttggc aggtgcagcc cccactgcct ttgacctgcc tcccttcatg				1491
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<400> 20

Met	Asp	Asn	Val	Leu	Pro	Val	Asp	Ser	Asp	Leu	Ser	Pro	Asn	Ile	Ser
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20 25 30

Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
35 40 45

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser
340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser
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Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser
385 390 395 400

Phe Ser Ser Asn Val Leu Ser
405

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atg gcc tcc agg ctg acc ctg ctg acc ctc ctg ctg ctg ctg gct 108

225	230	235	240	
cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt gac				828
Arg Thr Leu Tyr	Ser Ser Ser Pro Arg	Val Leu Ser Asn Asn Ser Asp		
	245	250	255	
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac				876
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn				
	260	265	270	
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc				924
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val				
	275	280	285	
ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt gat				972
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp				
	290	295	300	
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata				1020
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile				
	305	310	315	320
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att				1068
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile				
	325	330	335	
gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat				1116
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn				
	340	345	350	
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa				1164
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu				
	355	360	365	
gac atg gaa cag gct ctc agc cct tct gtt ttc aag gcc atc atg gag				1212
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu				
	370	375	380	
aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc				1260
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg				
	385	390	395	400
atc aaa gtg acg acc agc cag gat atg ctc tca atc atg gag aaa ttg				1308
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu				
	405	410	415	
gaa ttc ttc gat ttt tct tat gac ctt aac ctg tgt ggg ctg aca gag				1356
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu				
	420	425	430	
gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa				1404
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu				
	435	440	445	
ctg aca gag act ggg gtg gag gcg gct gca gcc tcc gcc atc tct gtg				1452
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val				
	450	455	460	

gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc gtg 1500
 Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
 465 470 475 480

ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat 1548
 Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
 485 490 495

gac ccc agg gcc tgagacctgc aggatcaggt tagggcgagc gctacctctc 1600
 Asp Pro Arg Ala
 500

cagcctcagc tctcagttgc agccctgctg ctgcctgcct ggacttgccc ctgccacctc 1660

ctgcctcagg tgtccgctat ccaccaaag ggctcctgag ggtctgggca agggacctgc 1720

ttctattagc ccttctccat ggccctgcc tgcctctcaa accacttttt gcagctttct 1780

ctagttcaag ttcaccagac tctataaata aaacctgaca gaccat 1826

<210> 22
 <211> 500
 <212> PRT
 <213> homo sapiens

<400> 22

Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala
 1 5 10 15

Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln
 20 25 30

Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr
 35 40 45

Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
 50 55 60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
 65 70 75 80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
 85 90 95

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
 100 105 110

Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
 115 120 125

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
 130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
 145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
 165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
 195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
 210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
 225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
 245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
 260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
 275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
 290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn

340	345	350
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu		
355	360	365
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu		
370	375	380
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg		
385	390	395 400
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu		
405	410	415
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu		
420	425	430
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu		
435	440	445
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val		
450	455	460
Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val		
465	470	475 480
Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr		
485	490	495
Asp Pro Arg Ala		
500		

<210> 23
 <211> 1826
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (61)..(1560)

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atg gcc tcc agg ctg acc ctg ctg acc ctc ctg ctg ctg ctg gct	108
Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Ala	


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gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc gtg      1500
Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
465                      470                      475                      480

ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat      1548
Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
                      485                      490                      495

gac ccc agg gcc tgagacctgc aggatcaggt tagggcgagc gctacctctc      1600
Asp Pro Arg Ala
                    500

cagcctcagc tctcagttgc agccctgctg ctgcctgcct ggacttgccc ctgccacctc      1660

ctgcctcagg tgtccgctat ccaccaaaag ggctcctgag ggtctgggca agggacctgc      1720

ttctattagc ccttctccat ggccctgcc tgcctctcaa accacttttt gcagctttct      1780

ctagttcaag ttcaccagac tctataaata aaacctgaca gaccat      1826

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<210> 24
<211> 500
<212> PRT
<213> homo sapiens

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<400> 24

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Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala
1                      5                      10                      15

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Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln
                20                25                30

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Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr
35                40                45

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```

Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
50                55                60

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```

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
65                70                75                80

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Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
85                90                95

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```

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
100                105                110

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Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr

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115

120

125

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
 130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
 145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
 165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
 195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
 210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
 225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
 245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
 260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
 275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
 290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
 340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
 355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
 370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
 385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
 405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
 420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
 435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val
 450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
 465 470 475 480

Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
 485 490 495

Asp Pro Arg Ala
 500

<210> 25
 <211> 1826
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (61)..(1560)

<400> 25
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atg gcc tcc agg ctg acc ctg ctg acc ctc ctg ctg ctg ctg gct 108
 Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Ala
 1 5 10 15

ggg gat aga gcc tcc tca aat cca aat gct acc agc tcc agc tcc cag	156
Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Gln	
20 25 30	
gat cca gag agt ttg caa gac aga ggc gaa ggg aag gtc gca aca aca	204
Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr	
35 40 45	
gtt atc tcc aag atg cta ttc gct gaa ccc atc ctg gag gtt tcc agc	252
Val Ile Ser Lys Met Leu Phe Ala Glu Pro Ile Leu Glu Val Ser Ser	
50 55 60	
ttg ccg aca acc aac tca aca acc aat tca gcc acc aaa ata aca gct	300
Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala	
65 70 75 80	
aat acc act gat gaa ccc acc aca caa ccc acc aca gag ccc acc acc	348
Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr	
85 90 95	
caa ccc acc atc caa ccc acc caa cca act acc cag ctc cca aca gat	396
Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp	
100 105 110	
tct cct acc cag ccc act act ggg tcc ttc tgc cca gga cct gtt act	444
Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr	
115 120 125	
ctc tgc tct gac ttg gag agt cat tca aca gag gcc gtg ttg ggg gat	492
Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp	
130 135 140	
gct ttg gta gat ttc tcc ctg aag ctc tac cac gcc ttc tca gca atg	540
Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met	
145 150 155 160	
aag aag gtg gag acc aac atg gcc ttt tcc cca ttc agc atc gcc agc	588
Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser	
165 170 175	
ctc ctt acc cag gtc ctg ctc ggg gct ggg cag aac acc aaa aca aac	636
Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn	
180 185 190	
ctg gag agc atc ctc tct tac ccc aag gac ttc acc tgt gtc cac cag	684
Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln	
195 200 205	
gcc ctg aag ggc ttc acg acc aaa ggt gtc acc tca gtc tct cag atc	732
Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile	
210 215 220	
ttc cac agc cca gac ctg gcc ata agg gac acc ttt gtg aat gcc tct	780
Phe His Ser Pro Asp Leu Ala Ile Arg Asp Phe Val Asn Ala Ser	
225 230 235 240	

cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt gac	828
Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp	
245 250 255	
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac	876
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn	
260 265 270	
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc	924
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val	
275 280 285	
ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt gat	972
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp	
290 295 300	
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata	1020
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile	
305 310 315 320	
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att	1068
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile	
325 330 335	
gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat	1116
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn	
340 345 350	
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa	1164
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu	
355 360 365	
gac atg gaa cag gct ctc agc cct tct gtt ttc aag gcc atc atg gag	1212
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu	
370 375 380	
aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc	1260
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg	
385 390 395 400	
atc aaa gtg acg acc agc cag gat atg ctc tca atc atg gag aaa ttg	1308
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu	
405 410 415	
gaa ttc ttc gat ttt tct tat gac ctt aac ctg tgt ggg ctg aca gag	1356
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu	
420 425 430	
gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa	1404
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu	
435 440 445	
ctg aca gag act ggg gtg gag gcg gct gca gcc tcc gcc atc tct gtg	1452
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val	
450 455 460	
gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc gtg	1500

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
 130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
 145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
 165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
 195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
 210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
 225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
 245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
 260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
 275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
 290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
 340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
 355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
 370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
 385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
 405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
 420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
 435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val
 450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
 465 470 475 480

Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
 485 490 495

Asp Pro Arg Ala
 500

<210> 27
 <211> 1826
 <212> DNA
 <213> homo sapiens

<220>
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 <222> (61)..(1560)

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atg gcc tcc agg ctg acc ctg ctg acc ctc ctg ctg ctg ctg gct 108
 Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala
 1 5 10 15

ggg gat aga gcc tcc tca aat cca aat gct acc agc tcc agc tcc cag	156
Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln	
20 25 30	
gat cca gag agt ttg caa gac aga ggc gaa ggg aag gtc gca aca aca	204
Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr	
35 40 45	
gtt atc tcc aag atg cta ttc gtt gaa ccc atc ctg gag gtt tcc agc	252
Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser	
50 55 60	
ttg ccg aca acc aac tca aca acc aat tca gcc acc aaa ata aca gct	300
Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala	
65 70 75 80	
aat acc act gat gaa ccc acc aca caa ccc acc aca gag ccc acc acc	348
Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr	
85 90 95	
caa ccc acc atc caa ccc acc caa cca act acc cag ctc cca aca gat	396
Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp	
100 105 110	
tct cct acc cag ccc act act ggg tcc ttc tgc cca gga cct gtt act	444
Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr	
115 120 125	
ctc tgc tct gac ttg gag agt cat tca aca gag gcc gtg ttg ggg gat	492
Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp	
130 135 140	
gct ttg gta gat ttc tcc ctg aag ctc tac cac gcc ttc tca gga atg	540
Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Gly Met	
145 150 155 160	
aag aag gtg gag acc aac atg gcc ttt tcc cca ttc agc atc gcc agc	588
Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser	
165 170 175	
ctc ctt acc cag gtc ctg ctc ggg gct ggg cag aac acc aaa aca aac	636
Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn	
180 185 190	
ctg gag agc atc ctc tct tac ccc aag gac ttc acc tgt gtc cac cag	684
Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln	
195 200 205	
gcc ctg aag ggc ttc acg acc aaa ggt gtc acc tca gtc tot cag atc	732
Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile	
210 215 220	
ttc cac agc cca gac ctg gcc ata agg gac acc ttt gtg aat gcc tct	780
Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser	
225 230 235 240	
cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt gac	828

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp	
245 250 255	
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac	876
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn	
260 265 270	
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc	924
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val	
275 280 285	
ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt gat	972
Leu Leu Asn Ala Ile Tyr Ser Ala Lys Trp Lys Thr Thr Phe Asp	
290 295 300	
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata	1020
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile	
305 310 315 320	
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att	1068
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile	
325 330 335	
gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat	1116
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn	
340 345 350	
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa	1164
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu	
355 360 365	
gac atg gaa cag gct ctc agc cct tct gtt ttc aag gcc atc atg gag	1212
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu	
370 375 380	
aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc	1260
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg	
385 390 395 400	
atc aaa gtg acg acc agc cag gat atg ctc tca atc atg gag aaa ttg	1308
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu	
405 410 415	
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Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu	
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gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa	1404
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu	
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Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val	
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Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val	

465 470 475 480
 ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat 1548
 Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
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 gac ccc agg gcc tgagacctgc aggatcaggt tagggcgagc gctacctctc 1600
 Asp Pro Arg Ala
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 cagcctcagc tctcagttgc agccctgctg ctgcctgcct ggacttgccc ctgccacctc 1660
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 Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
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 Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
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 Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
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 Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
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 Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
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Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
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Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Gly Met
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Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
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Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
 195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
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Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
 225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
 245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
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Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
 275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
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Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
 340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
 355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
 370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
 385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
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Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
 420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
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Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val
 450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
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 ggg gat aga gcc tcc tca aat cca aat gct acc agc tcc agc tcc cag 156

Gly	Asp	Arg	Ala	Ser	Ser	Asn	Pro	Asn	Ala	Thr	Ser	Ser	Ser	Ser	Gln		
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gat	cca	gag	agt	ttg	caa	gac	aga	ggc	gaa	ggg	aag	gtc	gca	aca	aca		204
Asp	Pro	Glu	Ser	Leu	Gln	Asp	Arg	Gly	Glu	Gly	Lys	Val	Ala	Thr	Thr		
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Val	Ile	Ser	Lys	Met	Leu	Phe	Val	Glu	Pro	Ile	Leu	Glu	Val	Ser	Ser		
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Leu	Pro	Thr	Thr	Asn	Ser	Thr	Thr	Asn	Ser	Ala	Thr	Lys	Ile	Thr	Ala		
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aat	acc	act	gat	gaa	ccc	acc	aca	caa	ccc	acc	aca	gag	ccc	acc	acc		348
Asn	Thr	Thr	Asp	Glu	Pro	Thr	Thr	Gln	Pro	Thr	Thr	Glu	Pro	Thr	Thr		
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Gln	Pro	Thr	Ile	Gln	Pro	Thr	Gln	Pro	Thr	Thr	Gln	Leu	Pro	Thr	Asp		
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Ser	Pro	Thr	Gln	Pro	Thr	Thr	Gly	Ser	Phe	Cys	Pro	Gly	Pro	Val	Thr		
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Leu	Cys	Ser	Asp	Leu	Glu	Ser	His	Ser	Thr	Glu	Ala	Val	Leu	Gly	Asp		
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Ala	Leu	Val	Asp	Phe	Ser	Leu	Lys	Leu	Tyr	His	Ala	Phe	Ser	Ala	Met		
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Lys	Lys	Val	Glu	Thr	Asn	Met	Ala	Phe	Ser	Pro	Phe	Ser	Ile	Ala	Ser		
				165				170						175			
ctc	ctt	acc	cag	gtc	ctg	ctc	ggg	gct	ggg	cag	aac	acc	aaa	aca	aac		636
Leu	Leu	Thr	Gln	Val	Leu	Leu	Gly	Ala	Gly	Gln	Asn	Thr	Lys	Thr	Asn		
			180					185						190			
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Leu	Glu	Ser	Ile	Leu	Ser	Tyr	Pro	Lys	Asp	Phe	Thr	Cys	Val	His	Gln		
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Ala	Leu	Lys	Gly	Phe	Thr	Thr	Lys	Gly	Val	Thr	Ser	Val	Ser	Gln	Ile		
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Phe	His	Ser	Pro	Asp	Leu	Ala	Ile	Arg	Asp	Thr	Phe	Val	Asn	Ala	Ser		
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Arg	Thr	Leu	Tyr	Ser	Ser	Ser	Pro	Arg	Val	Leu	Ser	Asn	Asn	Ser	Asp		

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Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp																				
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Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile																				
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Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu																				
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Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu																				
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Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val																				
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Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Met																				
465 470 475 480																				

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 Asp Pro Arg Ala
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Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
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Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
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Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
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Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
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Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
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Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
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Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
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Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
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Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
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Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
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Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
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Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
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Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
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Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
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Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
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Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
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Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
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Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
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Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
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Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu

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Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu		
370	375	380
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg		
385	390	400
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu		
	405	410
		415
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu		
	420	425
		430
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu		
	435	440
		445
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val		
	450	455
		460
Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Met		
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Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly Ala Ala Pro Pro Ile Gln	
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Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Gln His Ser Gln Pro Trp	
25 30 35	
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Gln Ala Ala Leu Tyr His Phe Ser Thr Phe Gln Cys Gly Gly Ile Leu	
40 45 50	
gtg cac cgc cag tgg gtg ctc aca gct gct cat tgc atc agc gac aat	246
Val His Arg Gln Trp Val Leu Thr Ala Ala His Cys Ile Ser Asp Asn	
55 60 65 70	
tac cag ctc tgg ctg ggt cgc cac aac ttg ttt gac gac gaa aac aca	294
Tyr Gln Leu Trp Leu Gly Arg His Asn Leu Phe Asp Asp Glu Asn Thr	
75 80 85	
gcc cag ttt gtt cat gtc agt gag agc ttc cca cac cct ggc ttc aac	342
Ala Gln Phe Val His Val Ser Glu Ser Phe Pro His Pro Gly Phe Asn	
90 95 100	
atg agc ctc ctg gag aac cac acc cgc caa gca gac gag gac tac agc	390
Met Ser Leu Leu Glu Asn His Thr Arg Gln Ala Asp Glu Asp Tyr Ser	
105 110 115	
cac gac ctc atg ctg ctc cgc ctg aca gag cct gct gat acc atc aca	438
His Asp Leu Met Leu Leu Arg Leu Thr Glu Pro Ala Asp Thr Ile Thr	
120 125 130	
gat gct gtg aag gtc gtg gag ttg ccc acc gag gaa ccc gaa gtg ggg	486
Asp Ala Val Lys Val Val Glu Leu Pro Thr Glu Glu Pro Glu Val Gly	
135 140 145 150	
agc acc tgt ttg gct tcc ggc tgg ggc agc atc gaa cca gag aat ttc	534
Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Asn Phe	
155 160 165	
tca ttt cca gat gat ctc cag tgt gtg gac ctc aaa atc ctg cct aat	582
Ser Phe Pro Asp Asp Leu Gln Cys Val Asp Leu Lys Ile Leu Pro Asn	
170 175 180	
gat gag tgc aaa aaa gcc cac gtc cag aag gtg aca gac ttc atg ctg	630
Asp Glu Cys Lys Lys Ala His Val Gln Lys Val Thr Asp Phe Met Leu	
185 190 195	
tgt gtc gga cac ctg gaa ggt ggc aaa gac acc tgt gtg ggt gat tca	678
Cys Val Gly His Leu Glu Gly Gly Lys Asp Thr Cys Val Gly Asp Ser	
200 205 210	
ggg ggc ccg ctg atg tgt gat ggt gtg ctc caa ggt gtc aca tca tgg	726
Gly Gly Pro Leu Met Cys Asp Gly Val Leu Gln Gly Val Thr Ser Trp	
215 220 225 230	
ggc tac gtc cct tgt ggc acc ccc aat aag cct tct gtc gcc gtc aga	774
Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys Pro Ser Val Ala Val Arg	
235 240 245	
gtg ctg tct tat gtg aag tgg atc gag gac acc ata gcg gag aac tcc	822

Val Leu Ser Tyr Val Lys Trp Ile Glu Asp Thr Ile Ala Glu Asn Ser
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 35 40 45

Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala
 50 55 60

His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu
 65 70 75 80

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe
 85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
 100 105 110

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
 115 120 125

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr
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Glu Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
 145 150 155 160

Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
 165 170 175

Leu Lys Ile Leu Pro Asn Asp Glu Cys Lys Lys Ala His Val Gln Lys
 180 185 190
 Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
 195 200 205
 Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
 210 215 220
 Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
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 Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Gln His Ser Gln Pro Trp
 25 30 35
 cag gcg gct ctg tac cat ttc agc act ttc cag tgt ggg ggc atc ctg 198
 Gln Ala Ala Leu Tyr His Phe Ser Thr Phe Gln Cys Gly Gly Ile Leu
 40 45 50
 gtg cac cgc cag tgg gtg ctc aca gct gct cat tgc atc agc gac aat 246
 Val His Arg Gln Trp Val Leu Thr Ala Ala His Cys Ile Ser Asp Asn
 55 60 65 70
 tac cag ctc tgg ctg ggt cgc cac aac ttg ttt gac gac gaa aac aca 294
 Tyr Gln Leu Trp Leu Gly Arg His Asn Leu Phe Asp Asp Glu Asn Thr
 75 80 85

gcc cag ttt gtt cat gtc agt gag agc ttc cca cac cct ggc ttc aac	342
Ala Gln Phe Val His Val Ser Glu Ser Phe Pro His Pro Gly Phe Asn	
90 95 100	
atg agc ctc ctg gag aac cac acc cgc caa gca gac gag gac tac agc	390
Met Ser Leu Leu Glu Asn His Thr Arg Gln Ala Asp Glu Asp Tyr Ser	
105 110 115	
cac gac ctc atg ctg ctc cgc ctg aca gag cct gct gat acc atc aca	438
His Asp Leu Met Leu Leu Arg Leu Thr Glu Pro Ala Asp Thr Ile Thr	
120 125 130	
gat gct gtg aag gtc gtg gag ttg ccc acc gag gaa ccc gaa gtg ggg	486
Asp Ala Val Lys Val Val Glu Leu Pro Thr Glu Glu Pro Glu Val Gly	
135 140 145 150	
agc acc tgt ttg gct tcc ggc tgg ggc agc atc gaa cca gag aat ttc	534
Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Asn Phe	
155 160 165	
tca ttt cca gat gat ctc cag tgt gtg gac ctc aaa atc ctg cct aat	582
Ser Phe Pro Asp Asp Leu Gln Cys Val Asp Leu Lys Ile Leu Pro Asn	
170 175 180	
gat gag tgc gaa aaa gcc cac gtc cag aag gtg aca gac ttc atg ctg	630
Asp Glu Cys Glu Lys Ala His Val Gln Lys Val Thr Asp Phe Met Leu	
185 190 195	
tgt gtc gga cac ctg gaa ggt ggc aaa gac acc tgt gtg ggt gat tca	678
Cys Val Gly His Leu Glu Gly Gly Lys Asp Thr Cys Val Gly Asp Ser	
200 205 210	
ggg ggc ccg ctg atg tgt gat ggt gtg ctc caa ggt gtc aca tca tgg	726
Gly Gly Pro Leu Met Cys Asp Gly Val Leu Gln Gly Val Thr Ser Trp	
215 220 225 230	
ggc tac gtc cct tgt ggc acc ccc aat aag cct tct gtc gcc gtc aga	774
Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys Pro Ser Val Ala Val Arg	
235 240 245	
gtg ctg tct tat gtg aag tgg atc gag gac acc ata gcg gag aac tcc	822
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Gln	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Tyr	His	Phe	Ser	Thr	Phe
		35					40					45			
Gln	Cys	Gly	Gly	Ile	Leu	Val	His	Arg	Gln	Trp	Val	Leu	Thr	Ala	Ala
	50					55					60				
His	Cys	Ile	Ser	Asp	Asn	Tyr	Gln	Leu	Trp	Leu	Gly	Arg	His	Asn	Leu
65					70					75					80
Phe	Asp	Asp	Glu	Asn	Thr	Ala	Gln	Phe	Val	His	Val	Ser	Glu	Ser	Phe
				85					90					95	
Pro	His	Pro	Gly	Phe	Asn	Met	Ser	Leu	Leu	Glu	Asn	His	Thr	Arg	Gln
			100					105					110		
Ala	Asp	Glu	Asp	Tyr	Ser	His	Asp	Leu	Met	Leu	Leu	Arg	Leu	Thr	Glu
		115					120					125			
Pro	Ala	Asp	Thr	Ile	Thr	Asp	Ala	Val	Lys	Val	Val	Glu	Leu	Pro	Thr
	130					135					140				
Glu	Glu	Pro	Glu	Val	Gly	Ser	Thr	Cys	Leu	Ala	Ser	Gly	Trp	Gly	Ser
145					150					155					160
Ile	Glu	Pro	Glu	Asn	Phe	Ser	Phe	Pro	Asp	Asp	Leu	Gln	Cys	Val	Asp
				165					170					175	
Leu	Lys	Ile	Leu	Pro	Asn	Asp	Glu	Cys	Glu	Lys	Ala	His	Val	Gln	Lys
			180					185					190		
Val	Thr	Asp	Phe	Met	Leu	Cys	Val	Gly	His	Leu	Glu	Gly	Gly	Lys	Asp
		195					200					205			
Thr	Cys	Val	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Asp	Gly	Val	Leu
	210					215					220				
Gln	Gly	Val	Thr	Ser	Trp	Gly	Tyr	Val	Pro	Cys	Gly	Thr	Pro	Asn	Lys
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Thr Ile Ala Glu Asn Ser
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 Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly Ala Ala Pro Pro Ile Gln
 10 15 20

tcc cgg att gtg gga ggc tgg gag tgt gag cag cat tcc cag ccc tgg 150
 Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Gln His Ser Gln Pro Trp
 25 30 35

cag gcg gct ctg tac cat ttc agc act ttc cag tgt ggg ggc atc ctg 198
 Gln Ala Ala Leu Tyr His Phe Ser Thr Phe Gln Cys Gly Gly Ile Leu
 40 45 50

gtg cac cgc cag tgg gtg ctc aca gct gct cat tgc atc agc gac aat 246
 Val His Arg Gln Trp Val Leu Thr Ala Ala His Cys Ile Ser Asp Asn
 55 60 65 70

tac cag ctc tgg ctg ggt cgc cac aac ttg ttt gac gac gaa aac aca 294
 Tyr Gln Leu Trp Leu Gly Arg His Asn Leu Phe Asp Asp Glu Asn Thr
 75 80 85

gcc cag ttt gtt cat gtc agt gag agc ttc cca cac cct ggc ttc aac 342
 Ala Gln Phe Val His Val Ser Glu Ser Phe Pro His Pro Gly Phe Asn
 90 95 100

atg agc ctc ctg gag aac cac acc cgc caa gca gac gag gac tac agc 390
 Met Ser Leu Leu Glu Asn His Thr Arg Gln Ala Asp Glu Asp Tyr Ser
 105 110 115

cac gac ctc atg ctg ctc cgc ctg aca gag cct gct gat acc atc aca 438
 His Asp Leu Met Leu Leu Arg Leu Thr Glu Pro Ala Asp Thr Ile Thr
 120 125 130

gat gct gtg aag gtc gtg gag ttg ccc acc cag gaa ccc gaa gtg ggg 486
 Asp Ala Val Lys Val Val Glu Leu Pro Thr Gln Glu Pro Glu Val Gly

135	140	145	150	
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Ser Thr Cys Leu	Ala Ser Gly Trp Gly	Ser Ile Glu Pro	Glu Asn Phe	
	155	160	165	
tca ttt cca gat gat ctc cag tgt gtg gac ctc aaa atc ctg cct aat				582
Ser Phe Pro Asp Asp Leu Gln Cys Val Asp Leu Lys Ile Leu Pro Asn				
	170	175	180	
gat gag tgc aaa aaa gcc cac gtc cag aag gtg aca gac ttc atg ctg				630
Asp Glu Cys Lys Lys Ala His Val Gln Lys Val Thr Asp Phe Met Leu				
	185	190	195	
tgt gtc gga cac ctg gaa ggt ggc aaa gac acc tgt gtg ggt gat tca				678
Cys Val Gly His Leu Glu Gly Gly Lys Asp Thr Cys Val Gly Asp Ser				
	200	205	210	
ggg ggc ccg ctg atg tgt gat ggt gtg ctc caa ggt gtc aca tca tgg				726
Gly Gly Pro Leu Met Cys Asp Gly Val Leu Gln Gly Val Thr Ser Trp				
	215	220	225	230
ggc tac gtc cct tgt ggc acc ccc aat aag cct tct gtc gcc gtc aga				774
Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys Pro Ser Val Ala Val Arg				
	235	240	245	
gtg ctg tct tat gtg aag tgg atc gag gac acc ata gcg gag aac tcc				822
Val Leu Ser Tyr Val Lys Trp Ile Glu Asp Thr Ile Ala Glu Asn Ser				
	250	255	260	
tgaacgccca gccctgtccc ctacccccag taaaatcaaaa tgtgcatcc				871
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Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu				
	20	25	30	
Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe				
	35	40	45	
Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala				
	50	55	60	
His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu				

65

70

75

80

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe
85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
100 105 110

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
115 120 125

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr
130 135 140

Gln Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
145 150 155 160

Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
165 170 175

Leu Lys Ile Leu Pro Asn Asp Glu Cys Lys Lys Ala His Val Gln Lys
180 185 190

Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
195 200 205

Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
210 215 220

Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
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ctgctgcaca gagtgtgcc aacatttatc atctccatct g 41

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tgttgttgtt gagacagggt ttcagtcggt cggcccagac t 41

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 atagtgtctag gattataggc atggccactg cgcctggccc c 41

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 caaatctgca gggctcccc gaccgcgccc aggtgggccc c 41

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<400> 256
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tgctgccagg gcccgagac acagcacagt tttttctcca g

41

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<212> DNA

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41

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<213> homo sapiens

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41

<210> 262

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<213> homo sapiens

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41

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41

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tatggagaca gactaggcaa attttgttta ataaatgagt g 41

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agcaggagag ccaggaccca tatgacacag atgaccactt t 41

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41

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<210> 281
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<400> 282
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41

<210> 283
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41

<210> 284
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<400> 284

cagactgtgt agcccaaggc agggatgggg actcctgcgt c 41

<210> 285
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<212> DNA
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<400> 285
aggtcgtgga gttgcccacc caggaacccg aagtggggag c 41

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<211> 41
<212> DNA
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<400> 286
ggcggggatg gggactcctg tgtccaaggg agaaagggcc a 41

<210> 287
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<213> homo sapiens

<400> 287
gggccacccc agctgtgtca gtctcatgcc tggaagtctg a 41

<210> 288
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<212> DNA
<213> homo sapiens

<400> 288
tgtcacgttc tgccatcacc catctttcca gatgtggtgc a 41

<210> 289
<211> 1082
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (956)..(956)
<223> wherein N is either a "G" or an "A".

<220>
<221> misc_feature
<222> (129)..(129)
<223> wherein N is either a "T" or a "C".

<220>


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Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
145                               150                               155                               160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
                               165                               170                               175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Xaa Leu
                               180                               185                               190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
                               195                               200                               205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
                               210                               215                               220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
225                               230                               235                               240

Xaa Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
                               245                               250                               255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
                               260                               265                               270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
                               275                               280                               285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
                               290                               295                               300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Xaa Leu Phe Arg
305                               310                               315                               320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
                               325                               330                               335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
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Asn

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<210> 291
<211> 1766
<212> DNA
<213> homo sapiens

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<220>
<221> CDS
<222> (211)..(1431)

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<220>
<221> misc_feature
<222> (543)..(543)
<223> wherein N is either a "T" or a "C".

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gtc	atn	tgg	gtc	ctg	gct	ctc	ctg	ctg	gcc	ttc	ccc	cag	ggc	tac	tac	714
Val	Xaa	Trp	Val	Leu	Ala	Leu	Leu	Leu	Ala	Phe	Pro	Gln	Gly	Tyr	Tyr	
		155					160					165				
tca	acc	aca	gag	acc	atg	ccc	agc	aga	gtc	gtg	tgc	atg	atc	gaa	tgg	762
Ser	Thr	Thr	Glu	Thr	Met	Pro	Ser	Arg	Val	Val	Cys	Met	Ile	Glu	Trp	
	170					175					180					
cca	gag	cat	ccg	aac	aag	att	tat	gag	aaa	gtg	tac	cac	atc	tgt	gtg	810
Pro	Glu	His	Pro	Asn	Lys	Ile	Tyr	Glu	Lys	Val	Tyr	His	Ile	Cys	Val	
185				190					195					200		
act	gtg	ctg	atc	tac	ttc	ctc	ccc	ctg	ctg	gtg	att	ggc	tat	gca	tac	858
Thr	Val	Leu	Ile	Tyr	Phe	Leu	Pro	Leu	Leu	Val	Ile	Gly	Tyr	Ala	Tyr	
			205					210					215			
acc	gta	gtg	gga	atc	aca	cta	tgg	gcc	agt	gag	atc	ccc	ggg	gac	tcc	906
Thr	Val	Val	Gly	Ile	Thr	Leu	Trp	Ala	Ser	Glu	Ile	Pro	Gly	Asp	Ser	
			220					225				230				
tct	gac	cgc	tac	cac	gag	caa	gtc	tct	gcc	aag	cgc	aag	gtg	gtc	aaa	954
Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys	
		235				240						245				
atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc	1002
Met	Met	Ile	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Phe	
	250					255					260					
cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag	1050
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys	
265				270					275					280		
aag	ttt	atc	cag	cag	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc	1098
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser	
			285					290						295		
tcc	acc	atg	tac	aac	ccc	atc	atc	tac	tgc	tgc	ctc	aat	gac	agg	ttc	1146
Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe	
			300					305					310			
cgt	ctg	ggc	ttc	aag	cat	gcc	ttc	cgg	tgc	tgc	ccc	ttc	atc	agc	gcc	1194
Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala	
		315				320						325				
ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc	1242
Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Lys	Ser	Thr	Arg	Tyr	Leu	Gln	Thr	
	330					335					340					
cag	ggc	agt	gtg	tac	aaa	gtc	agc	cgc	ctg	gag	acc	acc	atc	tcc	aca	1290
Gln	Gly	Ser	Val	Tyr	Lys	Val	Ser	Arg	Leu	Glu	Thr	Thr	Ile	Ser	Thr	
345					350				355					360		
gtg	gtg	ggg	gcc	cac	gag	gag	gag	cca	gag	gac	ggc	ccc	aag	gcc	aca	1338
Val	Val	Gly	Ala	His	Glu	Glu	Glu	Pro	Glu	Asp	Gly	Pro	Lys	Ala	Thr	

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
 50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
 65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
 85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Xaa Pro
 100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
 115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
 130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Xaa Trp Val Leu Ala Leu Leu
 145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
 165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
 180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
 195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
 210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
 225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
 245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
 260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu

275	280	285
Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile		
290	295	300
Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe		
305	310	315 320
Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met		
	325	330 335
Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser		
	340	345 350
Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu		
	355	360 365
Pro Glu Asp Gly Pro Lys Ala Thr Pro Xaa Ser Leu Asp Leu Thr Ser		
	370	375 380
Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser		
385	390	395 400
Phe Ser Ser Asn Val Leu Ser		
	405	

<210> 293
 <211> 1826
 <212> DNA
 <213> homo sapiens

<220>
 <221> misc_feature
 <222> (1278)..(1278)
 <223> wherein N is either a "C" or a "T".

<220>
 <221> misc_feature
 <222> (227)..(227)
 <223> wherein N is either a "T" or a "C".

<220>
 <221> misc_feature
 <222> (536)..(536)
 <223> wherein N is either a "C" or a "G".

<220>
 <221> misc_feature
 <222> (1498)..(1498)
 <223> wherein N is either a "G" or an "A".

<400> 293
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 atggcctcca ggctgaccct gctgaccctc ctgctgctgc tgctggctgg ggatagagcc 120
 tcctcaaadc caaatgctac cagctccagc tcccaggatc cagagagttt gcaagacaga 180
 ggcgaagggg aggtcgcaac aacagttatc tccaagatgc tattcgntga acccatcctg 240
 gaggtttcca gcttgccgac aaccaactca acaaccaatt cagccaccaa aataacagct 300
 aataccactg atgaaccac cacacaaccc accacagagc ccaccacca acccaccatc 360
 caaccacccc aaccaactac ccagctccca acagattctc ctaccagcc cactactggg 420
 tccttctgcc caggacctgt tactctctgc tctgacttgg agagtcattc aacagaggcc 480
 gtgttggggg atgctttggt agatttctcc ctgaagctct accacgcctt ctcagnaatg 540
 aagaaggtgg agaccaacat ggccttttcc ccattcagca tcgccagcct ccttaccag 600
 gtctgctcg gggctgggca gaacaccaa acaaacctgg agagcatcct ctcttaccac 660
 aaggacttca cctgtgtcca ccaggccctg aagggttca cgaccaaagg tgtcacctca 720
 gtctctcaga tcttcacag ccagacctg gccataaggg acaccttgt gaatgcctct 780
 cggaccctgt acagcagcag cccagagtc ctaagcaaca acagtgcgc caacttggag 840
 ctcatcaaca cctgggtggc caagaacacc aacaacaaga tcagccggct gctagacagt 900
 ctgccctccg ataccgcct tgctctctc aatgctatct acctgagtgc caagtggaag 960
 acaacatttg atcccaagaa aaccagaatg gaacctttc acttcaaaaa ctcagttata 1020
 aaagtgccca tgatgaatag caagaagtac cctgtggccc atttcattga ccaaactttg 1080
 aaagccaagg tggggcagct gcagctctcc cacaatctga gtttggtgat cctggtaccc 1140
 cagaacctga aacatcgtct tgaagacatg gaacaggctc tcagcccttc tgttttcaag 1200
 gccatcatgg agaaactgga gatgtccaag ttccagccca ctctcctaac actaccccg 1260
 atcaaagtga cgaccagnca ggatatgctc tcaatcatgg agaaattgga attcttcgat 1320
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 gccatctctg tggcccgcac cctgctggtc tttgaagtgc agcagccctt cctcttctg 1500

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tgagacctgc aggatcaggt tagggcgagc gctacctctc cagcctcagc tctcagttgc 1620
agccctgctg ctgcctgcct ggacttgccc ctgccacctc ctgcctcagg tgtccgctat 1680
ccacccaaaag ggctcctgag ggtctgggca agggacctgc ttctattagc ccttctccat 1740
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tctataaata aaacctgaca gaccat 1826

<210> 294
<211> 500
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (56)..(56)
<223> wherein Xaa is either "Val" or "Ala".

<220>
<221> VARIANT
<222> (159)..(159)
<223> wherein Xaa is either "Ala" or "Gly".

<220>
<221> VARIANT
<222> (480)..(480)
<223> wherein Xaa is either "Val" or "Met".

<400> 294

Met	Ala	Ser	Arg	Leu	Thr	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Ala
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Gly	Asp	Arg	Ala	Ser	Ser	Asn	Pro	Asn	Ala	Thr	Ser	Ser	Ser	Gln
			20					25					30	
Asp	Pro	Glu	Ser	Leu	Gln	Asp	Arg	Gly	Glu	Gly	Lys	Val	Ala	Thr
		35					40					45		
Val	Ile	Ser	Lys	Met	Leu	Phe	Xaa	Glu	Pro	Ile	Leu	Glu	Val	Ser
	50					55					60			
Leu	Pro	Thr	Thr	Asn	Ser	Thr	Thr	Asn	Ser	Ala	Thr	Lys	Ile	Thr
65				70				75						80
Asn	Thr	Thr	Asp	Glu	Pro	Thr	Thr	Gln	Pro	Thr	Thr	Glu	Pro	Thr
				85				90						95

<221> misc_feature
 <222> (348)..(348)
 <223> wherein N is either a "C" or a "T".

<220>
 <221> misc_feature
 <222> (462)..(462)
 <223> wherein N is either a "G" or an "A".

<220>
 <221> misc_feature
 <222> (577)..(577)
 <223> wherein N is either a "C" or a "G".

<220>
 <221> misc_feature
 <222> (705)..(705)
 <223> wherein N is either a "G" or an "A".

<400> 289
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 ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120
 gtgctgcna catttatcat ctccatctgt ttcttcggcc tcctagggaa cctttttgtc 180
 ctgttggtct tctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240
 ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300
 aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaangg ggtcatcaag 360
 gccaatattgt tcatcagcat cttcctggtg gtggccatca gccaggaccg ctaccgctg 420
 ctggtgcacc ctatggccag cggaaggcag cagcggcgga gncaggcccg ggtcacctgc 480
 gtgctcatct ggggttggtg gggcctcttg agcatcccca cattcctgct gcgatccatc 540
 caagccgtcc cagatctgaa catcacgcc tgcactntgc tcctcccca tgaggcctgg 600
 cactttgcaa ggattgtgga gttaaattt ctgggtttcc tcctaccact ggctgcgatc 660
 gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggangaggt cagcaggaca 720
 agagtgcngg ggccgaagga tagcaagacc acagcgctga tcctcacgct cgtggttgcc 780
 ttcttggtct gctgggcccc ttaccacttc ttgccttcc tggaattctt attccaggtg 840
 caagcagtc gaggctgctt ttgggaggac ttcatcgacc tgggcctgca attggccaac 900
 ttctttgcct tcaactaacag ctccctgaat ccagtaattt atgtctttgt gggcngctc 960
 ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020

Gln	Pro	Thr	Ile	Gln	Pro	Thr	Gln	Pro	Thr	Thr	Gln	Leu	Pro	Thr	Asp	
			100					105					110			
Ser	Pro	Thr	Gln	Pro	Thr	Thr	Gly	Ser	Phe	Cys	Pro	Gly	Pro	Val	Thr	
			115				120					125				
Leu	Cys	Ser	Asp	Leu	Glu	Ser	His	Ser	Thr	Glu	Ala	Val	Leu	Gly	Asp	
	130					135					140					
Ala	Leu	Val	Asp	Phe	Ser	Leu	Lys	Leu	Tyr	His	Ala	Phe	Ser	Xaa	Met	
145					150					155					160	
Lys	Lys	Val	Glu	Thr	Asn	Met	Ala	Phe	Ser	Pro	Phe	Ser	Ile	Ala	Ser	
				165					170					175		
Leu	Leu	Thr	Gln	Val	Leu	Leu	Gly	Ala	Gly	Gln	Asn	Thr	Lys	Thr	Asn	
			180					185					190			
Leu	Glu	Ser	Ile	Leu	Ser	Tyr	Pro	Lys	Asp	Phe	Thr	Cys	Val	His	Gln	
		195					200					205				
Ala	Leu	Lys	Gly	Phe	Thr	Thr	Lys	Gly	Val	Thr	Ser	Val	Ser	Gln	Ile	
	210					215						220				
Phe	His	Ser	Pro	Asp	Leu	Ala	Ile	Arg	Asp	Thr	Phe	Val	Asn	Ala	Ser	
225					230					235					240	
Arg	Thr	Leu	Tyr	Ser	Ser	Ser	Pro	Arg	Val	Leu	Ser	Asn	Asn	Ser	Asp	
				245					250					255		
Ala	Asn	Leu	Glu	Leu	Ile	Asn	Thr	Trp	Val	Ala	Lys	Asn	Thr	Asn	Asn	
			260					265					270			
Lys	Ile	Ser	Arg	Leu	Leu	Asp	Ser	Leu	Pro	Ser	Asp	Thr	Arg	Leu	Val	
		275					280					285				
Leu	Leu	Asn	Ala	Ile	Tyr	Leu	Ser	Ala	Lys	Trp	Lys	Thr	Thr	Phe	Asp	
	290					295					300					
Pro	Lys	Lys	Thr	Arg	Met	Glu	Pro	Phe	His	Phe	Lys	Asn	Ser	Val	Ile	
305					310					315					320	
Lys	Val	Pro	Met	Met	Asn	Ser	Lys	Lys	Tyr	Pro	Val	Ala	His	Phe	Ile	
				325					330					335		
Asp	Gln	Thr	Leu	Lys	Ala	Lys	Val	Gly	Gln	Leu	Gln	Leu	Ser	His	Asn	
			340					345					350			
Leu	Ser	Leu	Val	Ile	Leu	Val	Pro	Gln	Asn	Leu	Lys	His	Arg	Leu	Glu	
		355					360					365				
Asp	Met	Glu	Gln	Ala	Leu	Ser	Pro	Ser	Val	Phe	Lys	Ala	Ile	Met	Glu	
	370					375					380					
Lys	Leu	Glu	Met	Ser	Lys	Phe	Gln	Pro	Thr	Leu	Leu	Thr	Leu	Pro	Arg	
385					390					395					400	

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Xaa
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Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
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Asp Pro Arg Ala
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<223> wherein N is either an "A" or a "G".

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<222> (469)..(469)
<223> wherein N is either a "G" or a "C".

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tgggagtgtg agcagcattc ccagccctgg caggcggctc tgtaccattt cagcactttc 180

cagtgtgggg gcatcctggt gcaccgccag tgggtgctca cagctgctca ttgcatcagc 240

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<220>
<221> VARIANT
<222> (186)..(186)
<223> wherein Xaa is either "Lys" or "Glu".

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Gln	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Tyr	His	Phe	Ser	Thr	Phe				
			35				40					45							
Gln	Cys	Gly	Gly	Ile	Leu	Val	His	Arg	Gln	Trp	Val	Leu	Thr	Ala	Ala				
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His	Cys	Ile	Ser	Asp	Asn	Tyr	Gln	Leu	Trp	Leu	Gly	Arg	His	Asn	Leu				
65					70					75					80				
Phe	Asp	Asp	Glu	Asn	Thr	Ala	Gln	Phe	Val	His	Val	Ser	Glu	Ser	Phe				
				85					90					95					
Pro	His	Pro	Gly	Phe	Asn	Met	Ser	Leu	Leu	Glu	Asn	His	Thr	Arg	Gln				
			100					105					110						
Ala	Asp	Glu	Asp	Tyr	Ser	His	Asp	Leu	Met	Leu	Leu	Arg	Leu	Thr	Glu				
		115					120					125							
Pro	Ala	Asp	Thr	Ile	Thr	Asp	Ala	Val	Lys	Val	Val	Glu	Leu	Pro	Thr				

130 135 140
Xaa Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
145 150 155 160
Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
165 170 175
Leu Lys Ile Leu Pro Asn Asp Glu Cys Xaa Lys Ala His Val Gln Lys
180 185 190
Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
195 200 205
Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
210 215 220
Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
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tggc ag gaaa aat atg ga at c		21
<210> 532		
<211> 21		
<212> DNA		
<213> homo sapiens		
<400> 532		
g tag ctgcc aac ct t g act g		21
<210> 533		
<211> 21		
<212> DNA		
<213> homo sapiens		
<400> 533		
g ag ag ct tca g ct t ct c ct c c		21
<210> 534		
<211> 21		
<212> DNA		
<213> homo sapiens		
<400> 534		
g ag ag ct tca g ct t ct c ct c c		21

<210> 535
<211> 21
<212> DNA
<213> homo sapiens

<400> 535
gagagcttca gcttctcctc c 21

<210> 536
<211> 21
<212> DNA
<213> homo sapiens

<400> 536
agggtcacct cttcatctgc t 21

<210> 537
<211> 21
<212> DNA
<213> homo sapiens

<400> 537
tctgcagtcc atccctgata c 21

<210> 538
<211> 21
<212> DNA
<213> homo sapiens

<400> 538
accccaaaat gatgggacta c 21

<210> 539
<211> 21
<212> DNA
<213> homo sapiens

<400> 539
cctgggagta accctaagct g 21

<210> 540
<211> 21
<212> DNA
<213> homo sapiens

<400> 540
atctgttggg agctgggtag t 21

<210> 541

<211> 21
<212> DNA
<213> homo sapiens

<400> 541
gtccaacaaa tgacctggag a

21

<210> 542
<211> 21
<212> DNA
<213> homo sapiens

<400> 542
gagctgaggc tggagaggta g

21

<210> 543
<211> 21
<212> DNA
<213> homo sapiens

<400> 543
cctcaccaca caggtgtctt t

21

<210> 544
<211> 21
<212> DNA
<213> homo sapiens

<400> 544
cctcaccaca caggtgtctt t

21

<210> 545
<211> 21
<212> DNA
<213> homo sapiens

<400> 545
cctcaccaca caggtgtctt t

21

<210> 546
<211> 21
<212> DNA
<213> homo sapiens

<400> 546
cctcaccaca caggtgtctt t

21

<210> 547
<211> 21
<212> DNA
<213> homo sapiens

<400> 547		
gtgcaccaca tctggaaaga t		21
<210> 548		
<211> 21		
<212> DNA		
<213> homo sapiens		
<400> 548		
gtgcaccaca tctggaaaga t		21
<210> 549		
<211> 24		
<212> DNA		
<213> bacteriophage m13		
<400> 549		
agcggataac aatttcacac agga		24
<210> 550		
<211> 21		
<212> DNA		
<213> homo sapiens		
<400> 550		
agctcttcag gaccaaggtc t		21
<210> 551		
<211> 24		
<212> DNA		
<213> bacteriophage m13		
<400> 551		
cgccagggtt ttcccagtca cgac		24
<210> 552		
<211> 20		
<212> DNA		
<213> homo sapiens		
<400> 552		
ggcccacaaa gacataaatt		20
<210> 553		
<211> 8		
<212> PRT		
<213> Bacteriophage T7		
<400> 553		

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 554
<211> 733
<212> DNA
<213> homo sapiens

<400> 554
gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60
aattcgaggg tgcaccgtca gtcttctctt tcccccaaa acccaaggac accctcatga 120
tctcccgga tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgctgggtc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ccttcttctc ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggaaagtct tctcatgctc cgtgatgcat gaggctctgc 660
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat 733

<210> 555
<211> 1082
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (348)..(348)
<223> wherein N is either a "C" or a "T".

<400> 555
ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60
ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120
gtgctgccga catttatcat ctccatctgt ttcttcggcc tcttagggaa cctttttgtc 180
ctgttggtct tcctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240
ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300

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aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaatgg ggtcatcaag 360
gccaatttgt tcatcagcat ctccctgggtg gtggccatca gccaggaccg ctaccgcggtg 420
ctggtgcacc ctatggccag cggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480
gtgctcatct ggggttggtgg gggcctcttg agcatcccca cattcctgct gcgatccatc 540
caagccgtcc cagatctgaa catcacccgc tgcacccctgc tcctccccc tgaggcctgg 600
cactttgcaa ggattgtgga gttaaatatt ctgggtttcc tcctaccact ggctgcgatc 660
gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggaggagggt cagcaggaca 720
agagtgcggg ggccgaagga tagcaagacc acagcgctga tcctcacgct cgtgggttgcc 780
ttcctggtct gctgggcccc ttaccacttc tttgccttcc tggaattctt attccagggtg 840
caagcagtcc gaggctgctt ttgggaggac ttcattgacc tgggcctgca attggccaac 900
ttctttgcct tactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960
ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020
tcttcacccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080
cc 1082

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<210> 556
<211> 353
<212> PRT
<213> Homo sapiens

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```

<400> 556

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```

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
1          5          10          15

Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
20          25          30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
35          40          45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
50          55          60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
65          70          75          80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
85          90          95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
100         105         110

```

Ile	Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val
	115						120					125			
Val	Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Arg	Val	Leu	Val	His	Pro	Met	Ala
	130					135					140				
Ser	Gly	Arg	Gln	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Val	Thr	Cys	Val	Leu
145					150					155					160
Ile	Trp	Val	Val	Gly	Gly	Leu	Leu	Ser	Ile	Pro	Thr	Phe	Leu	Leu	Arg
				165					170					175	
Ser	Ile	Gln	Ala	Val	Pro	Asp	Leu	Asn	Ile	Thr	Ala	Cys	Ile	Leu	Leu
		180						185					190		
Leu	Pro	His	Glu	Ala	Trp	His	Phe	Ala	Arg	Ile	Val	Glu	Leu	Asn	Ile
		195					200					205			
Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Ile	Val	Phe	Phe	Asn	Tyr	His
	210					215					220				
Ile	Leu	Ala	Ser	Leu	Arg	Thr	Arg	Glu	Glu	Val	Ser	Arg	Thr	Arg	Val
225					230					235					240
Arg	Gly	Pro	Lys	Asp	Ser	Lys	Thr	Thr	Ala	Leu	Ile	Leu	Thr	Leu	Val
			245						250					255	
Val	Ala	Phe	Leu	Val	Cys	Trp	Ala	Pro	Tyr	His	Phe	Phe	Ala	Phe	Leu
		260						265					270		
Glu	Phe	Leu	Phe	Gln	Val	Gln	Ala	Val	Arg	Gly	Cys	Phe	Trp	Glu	Asp
		275					280					285			
Phe	Ile	Asp	Leu	Gly	Leu	Gln	Leu	Ala	Asn	Phe	Phe	Ala	Phe	Thr	Asn
	290					295					300				
Ser	Ser	Leu	Asn	Pro	Val	Ile	Tyr	Val	Phe	Val	Gly	Arg	Leu	Phe	Arg
305				310						315					320
Thr	Lys	Val	Trp	Glu	Leu	Tyr	Lys	Gln	Cys	Thr	Pro	Lys	Ser	Leu	Ala
			325						330					335	
Pro	Ile	Ser	Ser	Ser	His	Arg	Lys	Glu	Ile	Phe	Gln	Leu	Phe	Trp	Arg
			340					345					350		

Asn

<210> 557
 <211> 1082
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (462)..(462)

<223> wherein N is either a "G" or an "A".

<400> 557

ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60
ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctggggacct gctgcacaga 120
gtgctgccga catttatcat ctccatctgt ttcttcgggc tcttagggaa cctttttgtc 180
ctgttggtct tcctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240
ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300
aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360
gccaatttgt tcatcagcat ctctcctggtg gtggccatca gccaggaccg ctaccgctg 420
ctggtgcacc ctatggccag cggaaggcag cagcggcgga gacaggcccg ggtcacctgc 480
gtgctcatct gggttgtggg gggcctcttg agcatcccca cattcctgct gcgatccatc 540
caagccgtcc cagatctgaa catcaccgcc tgcactctgc tctccccca tgaggcctgg 600
cactttgcaa ggattgtgga gttaaataatt ctgggtttcc tcttaccact ggctgcgatc 660
gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggaggagggt cagcaggaca 720
agagtgcggg ggccgaagga tagcaagacc acagcgctga tcctcacgct cgtgggttgc 780
ttcctggtct gctgggcccc ttaccacttc tttgccttcc tggaattctt attccaggtg 840
caagcagtcc gaggtgctt ttggggaggac ttattgacc tgggcctgca attggccaac 900
ttctttgcct tcactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960
ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020
tcttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080
cc 1082

<210> 558

<211> 353

<212> PRT

<213> Homo sapiens

<400> 558

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
1 5 10 15
Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
20 25 30
Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys

35					40					45					
Phe	Phe	Gly	Leu	Leu	Gly	Asn	Leu	Phe	Val	Leu	Leu	Val	Phe	Leu	Leu
50						55					60				
Pro	Arg	Arg	Gln	Leu	Asn	Val	Ala	Glu	Ile	Tyr	Leu	Ala	Asn	Leu	Ala
65					70					75					80
Ala	Ser	Asp	Leu	Val	Phe	Val	Leu	Gly	Leu	Pro	Phe	Trp	Ala	Glu	Asn
				85					90					95	
Ile	Trp	Asn	Gln	Phe	Asn	Trp	Pro	Phe	Gly	Ala	Leu	Leu	Cys	Arg	Val
			100						105				110		
Ile	Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val
		115					120					125			
Val	Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Arg	Val	Leu	Val	His	Pro	Met	Ala
		130				135					140				
Ser	Gly	Arg	Gln	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Val	Thr	Cys	Val	Leu
145					150					155					160
Ile	Trp	Val	Val	Gly	Gly	Leu	Leu	Ser	Ile	Pro	Thr	Phe	Leu	Leu	Arg
				165					170					175	
Ser	Ile	Gln	Ala	Val	Pro	Asp	Leu	Asn	Ile	Thr	Ala	Cys	Ile	Leu	Leu
			180					185					190		
Leu	Pro	His	Glu	Ala	Trp	His	Phe	Ala	Arg	Ile	Val	Glu	Leu	Asn	Ile
		195					200					205			
Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Ile	Val	Phe	Phe	Asn	Tyr	His
		210				215					220				
Ile	Leu	Ala	Ser	Leu	Arg	Thr	Arg	Glu	Glu	Val	Ser	Arg	Thr	Arg	Val
225					230					235					240
Arg	Gly	Pro	Lys	Asp	Ser	Lys	Thr	Thr	Ala	Leu	Ile	Leu	Thr	Leu	Val
				245					250					255	
Val	Ala	Phe	Leu	Val	Cys	Trp	Ala	Pro	Tyr	His	Phe	Phe	Ala	Phe	Leu
			260					265					270		
Glu	Phe	Leu	Phe	Gln	Val	Gln	Ala	Val	Arg	Gly	Cys	Phe	Trp	Glu	Asp
		275					280					285			
Phe	Ile	Asp	Leu	Gly	Leu	Gln	Leu	Ala	Asn	Phe	Phe	Ala	Phe	Thr	Asn
		290				295					300				
Ser	Ser	Leu	Asn	Pro	Val	Ile	Tyr	Val	Phe	Val	Gly	Arg	Leu	Phe	Arg
305					310					315					320
Thr	Lys	Val	Trp	Glu	Leu	Tyr	Lys	Gln	Cys	Thr	Pro	Lys	Ser	Leu	Ala
				325					330					335	
Pro	Ile	Ser	Ser	Ser	His	Arg	Lys	Glu	Ile	Phe	Gln	Leu	Phe	Trp	Arg

340

345

350

Asn

<210> 559
 <211> 1082
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (577)..(577)
 <223> wherein N is either a "C" or a "G".

<400> 559
 ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60
 ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120
 gtgctgccga catttatcat ctccatctgt ttcttcgggc tcttagggaa cctttttgtc 180
 ctgttggtct tctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240
 ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300
 aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360
 gccaatttgt tcatcagcat ctctcctggtg gtggccatca gccaggaccg ctaccgcgtg 420
 ctggtgcacc ctatggccag cggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480
 gtgctcatct ggggttggtg gggcctcttg agcatcccca cattcctgct gcgatccatc 540
 caagccgtcc cagatctgaa catcacccgc tgcacgtgct tctcccccga tgaggcctgg 600
 cactttgcaa ggattgtgga gttaaattatt ctgggtttcc tcttaccact ggctgcgatc 660
 gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggaggagggt cagcaggaca 720
 agagtgcggg ggccgaagga tagcaagacc acagcgtgta tctcacgct cgtgggttgc 780
 ttcttggtct gctgggcccc ttaccacttc tttgccttcc tggaattctt attccaggtg 840
 caagcagtcc gaggtctgctt ttgggaggac ttcatcgacc tgggcctgca attggccaac 900
 ttctttgcct tactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960
 ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020
 tcttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080
 cc 1082

<210> 560

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
325 330 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
340 345 350

Asn

<210> 561
<211> 1082
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (705)..(705)
<223> wherein N is either a "G" or an "A".

<400> 561
ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60
ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120
gtgctgccga catttatcat ctccatctgt ttcttcgggc tcttagggaa cctttttgtc 180
ctgttggtct tctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240
ctggcagcct ctgatctggt gtttgtcttg ggcttgcct tctgggcaga gaatatctgg 300
aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360
gccaatttgt tcatcagcat ctctctggtg gtggccatca gccaggaccg ctaccgcgtg 420
ctgggtgcacc ctatggccag cggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480
gtgctcatct gggttgtggg gggcctcttg agcatcccca cattcctgct gcgatccatc 540
caagccgtcc cagatctgaa catcacgcc tgcactctgc tctccccca tgaggcctgg 600
cactttgcaa ggattgtgga gttaaattatt ctgggtttcc tctaccact ggctgcgatc 660

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gtctttcttca actaccacat cctggcctcc ctgcgaacgc gggaggaggt cagcaggaca 720
agagtgcggg ggccgaagga tagcaagacc acagcgctga tcctcacgct cgtgggttgcc 780
ttcctggtct gctggggcccc ttaccacttc ttgaccttc tggaattctt attccaggtg 840
caagcagtcc gaggtctgctt ttgggaggac ttcattgacc tgggcctgca attggccaac 900
ttctttgcct tcactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960
ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020
tcttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080
cc 1082

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<210> 562
<211> 353
<212> PRT
<213> Homo sapiens

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```
<400> 562
```

```

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
1          5          10          15

Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
20          25          30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
35          40          45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
50          55          60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
65          70          75          80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
85          90          95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
100         105         110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
115         120         125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
130         135         140

Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys Val Leu
145         150         155         160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
165         170         175

```

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
 180 185 190
 Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
 195 200 205
 Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
 210 215 220
 Ile Leu Ala Ser Leu Arg Thr Arg Lys Glu Val Ser Arg Thr Arg Val
 225 230 235 240
 Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
 245 250 255
 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
 260 265 270
 Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
 275 280 285
 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
 290 295 300
 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
 305 310 315 320
 Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
 325 330 335
 Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
 340 345 350

Asn

<210> 563
 <211> 3733
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (40)..(40)
 <223> wherein N is either a "C" or a "T".

<400> 563
 atgttctctc cctggaagat atcaatgttt ctgtctgttt gtgaggactc cgtgccacc 60
 acggcctctt tcagcgccga catgctcaat gtcaccttgc aagggccac tcttaacggg 120
 acctttgcc agagcaaagt cccccaagt gagtggtctg gctggctcaa caccatccag 180
 cccccccttc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc 240

gtcttctgcc	tgcacaagag	cagctgcacg	gtggcagaga	tctacctggg	gaacctggcc	300
gcagcagacc	tgatcctggc	ctgcgggctg	cccttctggg	ccatcaccat	ctccaacaac	360
ttcgactggc	tcttttggga	gacgctctgc	cgcggtggtga	atgccattat	ctccatgaac	420
ctgtacagca	gcatctgttt	cctgatgctg	gtgagcatcg	accgctacct	ggccctggtg	480
aaaaccatgt	ccatgggccc	gatgcgcggc	gtgcgctggg	ccaagctcta	cagcttggtg	540
atctgggggt	gtacgctgct	cctgagctca	cccatgctgg	tgttccggac	catgaaggag	600
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aagactcaag	tggsaacgac	tgggcactgc	caccaccaga	aagctgttcg	acgagacggt	1920
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aaaaaaaaaa aaa 3733

<210> 564

<211> 391

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (14)..(14)

<223> wherein Xaa is either "Arg" or "Cys".

<400> 564

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Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro
35 40 45

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser
130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val
145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu
165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met
180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val
195 200 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr
 210 215 220
 Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile
 225 230 235 240
 Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met
 245 250 255
 Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val
 260 265 270
 Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile
 275 280 285
 Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
 290 295 300
 Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
 305 310 315 320
 Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
 325 330 335
 Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
 340 345 350
 Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly
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<210> 565
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 ttcgactggc tctttgggga gacgctctgc cgcgtggtga atgccattat ctccatgaac 420
 ctgtacagca gcatctgttt cctgatgctg gtgagcatcg accgctacct ggccctggtg 480
 aaaaccatgt ccatgggccc gatgcgcggc gtgcgctggg ccaagctcta cagcttggtg 540
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 tacagcgatg agggccacaa cgtcaccgct tgtgtcatca gctacccatc cctcatctgg 660
 gaagtgttca ccaacatgct cctgaatgtc gtgggcttcc tgetgcccct gagtgtcatc 720
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 aagactcaag tgggaacgac tgggcaactgc caccaccaga aagctgttcg acgagacggt 1920
 cgagcagggt gctgtgggtg atatggacag cagaaggggg agaccaaggt tccagctcaa 1980

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<211> 391
<212> PRT
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35 40 45
Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
50 55 60
Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
65 70 75 80
Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
85 90 95
Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
100 105 110
Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125
Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser
130 135 140
Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val
145 150 155 160
Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu
165 170 175
Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met
180 185 190
Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val
195 200 205
Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr
210 215 220
Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile
225 230 235 240
Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met

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Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile
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Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
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Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
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Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
325 330 335
Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
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Asp Trp Ala Gly Ser Arg Gln
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<210> 567
<211> 3733
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1061)..(1061)
<223> wherein N is either a "G" or an "A".

<400> 567
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acctttgccc agagcaaatg cccccaagtg gagtggctgg gctgggtcaa caccatccag 180
cccccttcc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc 240
gtcttctgcc tgcacaagag cagctgcacg gtggcagaga tctacctggg gaacctggcc 300
gcagcagacc tgatcctggc ctgcgggctg cccttctggg ccatcaccat ctccaacaac 360
ttcgactggc tctttgggga gacgctctgc cgcgtggtga atgccattat ctccatgaac 420
ctgtacagca gcactgtttt cctgatgctg gtgagcatcg accgctacct ggcctgggtg 480

aagcaccagt gtctggcaca cagtaggtgc tcattggctc ccttccacct gtcattccca	2280
ccaccctgag gcccgaaccg ccacacacac aggagcattt ggagagaagg ccatgtcttc	2340
aaagtctgat ttgtgatgag gcagaggaag atattttctaa tcgggtcttgcc ccagaggatc	2400
acagtgtctga gacccccac caccagccgg tacctgggaa gggggagagt gcaggcctgc	2460
tcagggactg ttctgtgttc agcaaccaag ggattgttcc tgtcaatcaa tggtttattg	2520
gaagggtggcc cagtatgagc cctagaagag tgtgaaaagg aatggcaatg gtgttcacca	2580
tcggcagtgc cagggcagca ctcatcact tgataaatga atatttatta gctgggttga	2640
gagctagaac ctggagagct agaacctgga gaactagaac ctggagggct agaacctgga	2700
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aagggtctga acctggaggg ctggaatctg gagagctaga acctggaggg ctagaacctg	2940
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agaatgaagt caaactgtgc cacacatggg gaatgaaaaa aaaaaaaaag aggctgtgtt	3420
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gtgaaagact caatgagctg ttatgttgta aacaggaagc atttcacatc caaacgagaa	3660
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aaaaaaaaaa aaa	3733
<210> 568	
<211> 391	
<212> PRT	

<213> Homo sapiens

<220>

<221> VARIANT

<222> (354)..(354)

<223> wherein Xaa is either "Gly" or "Glu".

<400> 568

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Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr
20 25 30

Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro
35 40 45

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser
130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val
145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu
165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met
180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val
195 200 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr
210 215 220

Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile
225 230 235 240

Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met
245 250 255

Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val
260 265 270

Leu	Val	Val	Leu	Leu	Leu	Phe	Ile	Ile	Cys	Trp	Leu	Pro	Phe	Gln	Ile
		275					280					285			

Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
290 295 300

Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
305 310 315 320

Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
325 330 335

Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
340 345 350

Lys Glu Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly
355 360 365

Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln
370 375 380

Asp Trp Ala Gly Ser Arg Gln
385 390

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<210> 569
<211> 3405
<212> DNA
<213> Homo sapiens
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<400>	569									
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gctccttctc	agccttgttg	ctgtaactgc	tgctcagtc	accattgagg	aacaggccaa					180
gacatttttg	gacaagttta	accacgaagc	cgaagacctg	ttctatcaaa	gttcacttgc					240
ttcttggaat	tataaacacca	atattactga	agagaatgtc	caaaacatga	ataatgctgg					300
ggacaaatgg	tctgcctttt	taaaggaaca	gtccacactt	gcccaaatgt	atccactaca					360
agaaattcag	aatctcacag	tcaagcttca	gctgcaggct	cttcagcaaa	atgggtcttc					420
agtgcctcca	gaagacaaga	gcaaacgggt	gaacacaatt	ctaaatacaa	tgagcaccat					480
ctacagtact	ggaaaagttt	gtaaccgaga	taatccacaa	gaatgcttat	tacttgaacc					540
aggtttgaat	gaaataatgg	caaacagttt	agactacaat	gagaggctct	gggcttggha					600
aagctggaga	tctgaggtcg	gcaagcagct	gagggcatta	tatgaagagt	atgtgggtctt					660
gaaaaatgag	atggcaagag	caaatcatta	tgaggactat	ggggattatt	ggagaggaga					720

ctatgaagta aatggggtag atggctatga ctacagccgc ggccagttga ttgaagatgt	780
ggaacatacc tttgaagaga ttaaaccatt atatgaacat cttcatgcct atgtgagggc	840
aaagttgatg aatgcctatc cttcctatat cagtccaatt ggatgcctcc ctgctcattt	900
gcttgggtgat atgtggggta gattttggac aaatctgtac tctttgacag ttccttttgg	960
acagaaacca aacatagatg ttactgatgc aatggtggac caggcctggg atgcacagag	1020
aatattcaag gaggccgaga agttctttgt atctgttggg cttcctaata tgactcaagg	1080
attctgggaa aattccatgc taacggaccc aggaaatggt cagaaagcag tctgccatcc	1140
cacagcttgg gacctgggga agggcgactt caggatcctt atgtgcacaa aggtgacaat	1200
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gagtaccgac tggagtccat atgcagacca aagcatcaaa gtgaggataa gcctaaaatc	1980
agctcttggg gataaagcat atgaatggaa cgacaatgaa atgtacctgt tccgatcatc	2040
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gatacagcca acacttggac ctccaaacca gccccctgtt tccatatggc tgattgtttt	2340
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acccagtctc ttaaactctt tgtatttgct cacagtgttt gagcagtgtc gagcacaaag 3360
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<210> 570
<211> 805
<212> PRT
<213> Homo sapiens

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<400> 570
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Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala
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Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe
          20          25          30

Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp
          35          40          45

Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn
          50          55          60

Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala
65          70          75          80

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Gln	Met	Tyr	Pro	Leu	Gln	Glu	Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln	
				85					90					95		
Leu	Gln	Ala	Leu	Gln	Gln	Asn	Gly	Ser	Ser	Val	Leu	Ser	Glu	Asp	Lys	
				100					105					110		
Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser	
				115					120					125		
Thr	Gly	Lys	Val	Cys	Asn	Pro	Asp	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu	
				130					135					140		
Glu	Pro	Gly	Leu	Asn	Glu	Ile	Met	Ala	Asn	Ser	Leu	Asp	Tyr	Asn	Glu	
				145					150					155		
Arg	Leu	Trp	Ala	Trp	Glu	Ser	Trp	Arg	Ser	Glu	Val	Gly	Lys	Gln	Leu	
				165					170					175		
Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg	
				180					185					190		
Ala	Asn	His	Tyr	Glu	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu	
				195					200					205		
Val	Asn	Gly	Val	Asp	Gly	Tyr	Asp	Tyr	Ser	Arg	Gly	Gln	Leu	Ile	Glu	
				210					215					220		
Asp	Val	Glu	His	Thr	Phe	Glu	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu	
				225					230					235		
His	Ala	Tyr	Val	Arg	Ala	Lys	Leu	Met	Asn	Ala	Tyr	Pro	Ser	Tyr	Ile	
				245					250					255		
Ser	Pro	Ile	Gly	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly	
				260					265					270		
Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Ser	Leu	Thr	Val	Pro	Phe	Gly	Gln	Lys	
				275					280					285		
Pro	Asn	Ile	Asp	Val	Thr	Asp	Ala	Met	Val	Asp	Gln	Ala	Trp	Asp	Ala	
				290					295					300		
Gln	Arg	Ile	Phe	Lys	Glu	Ala	Glu	Lys	Phe	Phe	Val	Ser	Val	Gly	Leu	
				305					310					315		
Pro	Asn	Met	Thr	Gln	Gly	Phe	Trp	Glu	Asn	Ser	Met	Leu	Thr	Asp	Pro	
				325					330					335		
Gly	Asn	Val	Gln	Lys	Ala	Val	Cys	His	Pro	Thr	Ala	Trp	Asp	Leu	Gly	
				340					345					350		
Lys	Gly	Asp	Phe	Arg	Ile	Leu	Met	Cys	Thr	Lys	Val	Thr	Met	Asp	Asp	
				355					360					365		
Phe	Leu	Thr	Ala	His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Asp	Met	Ala	
				370					375					380		

Tyr	Ala	Ala	Gln	Pro	Phe	Leu	Leu	Arg	Asn	Gly	Ala	Asn	Glu	Gly	Phe	385	390	395	400
His	Glu	Ala	Val	Gly	Glu	Ile	Met	Ser	Leu	Ser	Ala	Ala	Thr	Pro	Lys	405	410	415	
His	Leu	Lys	Ser	Ile	Gly	Leu	Leu	Ser	Pro	Asp	Phe	Gln	Glu	Asp	Asn	420	425	430	
Glu	Thr	Glu	Ile	Asn	Phe	Leu	Leu	Lys	Gln	Ala	Leu	Thr	Ile	Val	Gly	435	440	445	
Thr	Leu	Pro	Phe	Thr	Tyr	Met	Leu	Glu	Lys	Trp	Arg	Trp	Met	Val	Phe	450	455	460	
Lys	Gly	Glu	Ile	Pro	Lys	Asp	Gln	Trp	Met	Lys	Lys	Trp	Trp	Glu	Met	465	470	475	480
Lys	Arg	Glu	Ile	Val	Gly	Val	Val	Glu	Pro	Val	Pro	His	Asp	Glu	Thr	485	490	495	
Tyr	Cys	Asp	Pro	Ala	Ser	Leu	Phe	His	Val	Ser	Asn	Asp	Tyr	Ser	Phe	500	505	510	
Ile	Arg	Tyr	Tyr	Thr	Arg	Thr	Leu	Tyr	Gln	Phe	Gln	Phe	Gln	Glu	Ala	515	520	525	
Leu	Cys	Gln	Ala	Ala	Lys	His	Glu	Gly	Pro	Leu	His	Lys	Cys	Asp	Ile	530	535	540	
Ser	Asn	Ser	Thr	Glu	Ala	Gly	Gln	Lys	Leu	Phe	Asn	Met	Leu	Arg	Leu	545	550	555	560
Gly	Lys	Ser	Glu	Pro	Trp	Thr	Leu	Ala	Leu	Glu	Asn	Val	Val	Gly	Ala	565	570	575	
Lys	Asn	Met	Asn	Val	Arg	Pro	Leu	Leu	Asn	Tyr	Phe	Glu	Pro	Leu	Phe	580	585	590	
Thr	Trp	Leu	Lys	Asp	Gln	Asn	Lys	Asn	Ser	Phe	Val	Gly	Trp	Ser	Thr	595	600	605	
Asp	Trp	Ser	Pro	Tyr	Ala	Asp	Gln	Ser	Ile	Lys	Val	Arg	Ile	Ser	Leu	610	615	620	
Lys	Ser	Ala	Leu	Gly	Asp	Lys	Ala	Tyr	Glu	Trp	Asn	Asp	Asn	Glu	Met	625	630	635	640
Tyr	Leu	Phe	Arg	Ser	Ser	Val	Ala	Tyr	Ala	Met	Arg	Gln	Tyr	Phe	Leu	645	650	655	
Lys	Val	Lys	Asn	Gln	Met	Ile	Leu	Phe	Gly	Glu	Glu	Asp	Val	Arg	Val	660	665	670	
Ala	Asn	Leu	Lys	Pro	Arg	Ile	Ser	Phe	Asn	Phe	Phe	Val	Thr	Ala	Pro	675	680	685	

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
 690 695 700
 Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
 705 710 715 720
 Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln
 725 730 735
 Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
 740 745 750
 Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
 755 760 765
 Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile
 770 775 780
 Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp
 785 790 795 800
 Val Gln Thr Ser Phe
 805

<210> 571
 <211> 1284
 <212> DNA
 <213> Homo sapiens

<400> 571
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 gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccctc 180
 cgcttctact acctgatcgc ttcgggagacc ccggggaaga acatcttttt ctccccgctg 240
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 gtcgtcgacc ccacgaaacc atag 1284

<210> 572
 <211> 427
 <212> PRT
 <213> Homo sapiens
 <400> 572

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 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
 35 40 45
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr
 50 55 60
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu
 65 70 75 80
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His
 85 90 95
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu
 100 105 110
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu
 115 120 125
 Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe
 130 135 140
 Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met
 145 150 155 160
 Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val
 165 170 175

Gly	Thr	Ile	Gln	Leu	Ile	Asn	Asp	His	Val	Lys	Lys	Glu	Thr	Arg	Gly	180	185	190
Lys	Ile	Val	Asp	Leu	Val	Ser	Glu	Leu	Lys	Lys	Asp	Val	Leu	Met	Val	195	200	205
Leu	Val	Asn	Tyr	Ile	Tyr	Phe	Lys	Ala	Leu	Trp	Glu	Lys	Pro	Phe	Ile	210	215	220
Ser	Ser	Arg	Thr	Thr	Pro	Lys	Asp	Phe	Tyr	Val	Asp	Glu	Asn	Thr	Thr	225	230	235
Val	Arg	Val	Pro	Met	Met	Leu	Gln	Asp	Gln	Glu	His	His	Trp	Tyr	Leu	245	250	255
His	Asp	Arg	Tyr	Leu	Pro	Cys	Ser	Val	Leu	Arg	Met	Asp	Tyr	Lys	Gly	260	265	270
Asp	Ala	Thr	Val	Phe	Phe	Ile	Leu	Pro	Asn	Gln	Gly	Lys	Met	Arg	Glu	275	280	285
Ile	Glu	Glu	Val	Leu	Thr	Pro	Glu	Met	Leu	Met	Arg	Trp	Asn	Asn	Leu	290	295	300
Leu	Arg	Lys	Arg	Asn	Phe	Tyr	Lys	Lys	Leu	Glu	Leu	His	Leu	Pro	Lys	305	310	315
Phe	Ser	Ile	Ser	Gly	Ser	Tyr	Val	Leu	Asp	Gln	Ile	Leu	Pro	Arg	Leu	325	330	335
Gly	Phe	Thr	Asp	Leu	Phe	Ser	Lys	Trp	Ala	Asp	Leu	Ser	Gly	Ile	Thr	340	345	350
Lys	Gln	Gln	Lys	Leu	Glu	Ala	Ser	Lys	Ser	Phe	His	Lys	Ala	Thr	Leu	355	360	365
Asp	Val	Asp	Glu	Ala	Gly	Thr	Glu	Ala	Ala	Ala	Ala	Thr	Thr	Phe	Ala	370	375	380
Ile	Lys	Phe	Phe	Ser	Ala	Gln	Thr	Asn	Arg	His	Ile	Leu	Arg	Phe	Asn	385	390	395
Arg	Pro	Phe	Leu	Val	Val	Ile	Phe	Ser	Thr	Ser	Thr	Gln	Ser	Val	Leu	405	410	415
Phe	Leu	Gly	Lys	Val	Val	Asp	Pro	Thr	Lys	Pro						420	425	

<210> 573
 <211> 1284
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (699)..(699)

<223> wherein N is either a "C" or a "T".

<400> 573

atgcatctta tcgactacct gtcctcctg ctggttggac tactggccct ttctcatggc 60
cagctgcacg ttgagcatga tggtagagagt tgcagtaaca gctccaccca gcagattctg 120
gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc 180
cgcttctact acctgatcgc ttcggagacc ccggggaaga acatcttttt ctccccgctg 240
agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300
atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360
ttccagcacc tcctgcacac tctcaacctc cccggccatg ggctggaaac acgcgtgggc 420
agtgtctgtt tcctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg 480
gccgtctatg aggctaaact cttccacacc aacttctacg aactgtggg cacaatccag 540
cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagttag 600
ctcaagaagg acgtcttgat ggtgctggtg aattacattt acttcaaagc cctgtgggag 660
aaaccattca tttcctcaag gaccactccc aaagactttt atgttgatga gaacacaaca 720
gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac 780
ttgccctgct cgggtgctacg gatggattac aaaggagacg caaccgtgtt tttcattctc 840
cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattgagg 900
tggaacaact tggtgcggaa gaggaatttt tacaagaagc tagagttgca tcttccaag 960
ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020
ctgttctcca agtgggctga cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080
aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140
accacgttcg cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200
cggcccttcc ttgtgggtgat cttttccacc agcaccacaga gtgtcctctt tctgggcaag 1260
gtcgtcgacc ccacgaaacc atag 1284

<210> 574

<211> 427

<212> PRT

<213> Homo sapiens

<400> 574

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala

1		5		10		15													
Leu	Ser	His	Gly	Gln	Leu	His	Val	Glu	His	Asp	Gly	Glu	Ser	Cys	Ser				
			20					25					30						
Asn	Ser	Ser	His	Gln	Gln	Ile	Leu	Glu	Thr	Gly	Glu	Gly	Ser	Pro	Ser				
		35					40					45							
Leu	Lys	Ile	Ala	Pro	Ala	Asn	Ala	Asp	Phe	Ala	Phe	Arg	Phe	Tyr	Tyr				
	50					55					60								
Leu	Ile	Ala	Ser	Glu	Thr	Pro	Gly	Lys	Asn	Ile	Phe	Phe	Ser	Pro	Leu				
65					70				75						80				
Ser	Ile	Ser	Ala	Ala	Tyr	Ala	Met	Leu	Ser	Leu	Gly	Ala	Cys	Ser	His				
				85				90						95					
Ser	Arg	Ser	Gln	Ile	Leu	Glu	Gly	Leu	Gly	Phe	Asn	Leu	Thr	Glu	Leu				
			100					105					110						
Ser	Glu	Ser	Asp	Val	His	Arg	Gly	Phe	Gln	His	Leu	Leu	His	Thr	Leu				
		115					120					125							
Asn	Leu	Pro	Gly	His	Gly	Leu	Glu	Thr	Arg	Val	Gly	Ser	Ala	Leu	Phe				
	130					135					140								
Leu	Ser	His	Asn	Leu	Lys	Phe	Leu	Ala	Lys	Phe	Leu	Asn	Asp	Thr	Met				
145					150					155					160				
Ala	Val	Tyr	Glu	Ala	Lys	Leu	Phe	His	Thr	Asn	Phe	Tyr	Asp	Thr	Val				
				165					170					175					
Gly	Thr	Ile	Gln	Leu	Ile	Asn	Asp	His	Val	Lys	Lys	Glu	Thr	Arg	Gly				
			180					185					190						
Lys	Ile	Val	Asp	Leu	Val	Ser	Glu	Leu	Lys	Lys	Asp	Val	Leu	Met	Val				
	195						200					205							
Leu	Val	Asn	Tyr	Ile	Tyr	Phe	Lys	Ala	Leu	Trp	Glu	Lys	Pro	Phe	Ile				
	210					215					220								
Ser	Ser	Arg	Thr	Thr	Pro	Lys	Asp	Phe	Tyr	Val	Asp	Glu	Asn	Thr	Thr				
225					230					235					240				
Val	Arg	Val	Pro	Met	Met	Leu	Gln	Asp	Gln	Glu	His	His	Trp	Tyr	Leu				
				245					250					255					
His	Asp	Arg	Tyr	Leu	Pro	Cys	Ser	Val	Leu	Arg	Met	Asp	Tyr	Lys	Gly				
		260						265					270						
Asp	Ala	Thr	Val	Phe	Phe	Ile	Leu	Pro	Asn	Gln	Gly	Lys	Met	Arg	Glu				
		275					280					285							
Ile	Glu	Glu	Val	Leu	Thr	Pro	Glu	Met	Leu	Met	Arg	Trp	Asn	Asn	Leu				
	290					295					300								
Leu	Arg	Lys	Arg	Asn	Phe	Tyr	Lys	Lys	Leu	Glu	Leu	His	Leu	Pro	Lys				

305 310 315 320
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
 325 330 335
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
 340 345 350
 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
 355 360 365
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
 370 375 380
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
 385 390 395 400
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
 405 410 415
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
 420 425

<210> 575
 <211> 1284
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (597)..(597)
 <223> wherein N is either a "T" or a "C".

<400> 575
 atgcattctta tcgactacct gctcctcctg ctggttggac tactggccct ttctcatggc 60
 cagctgcacg ttgagcatga tgggtgagagt tgcagtaaca gctcccacca gcagattctg 120
 gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc 180
 cgcttctact acctgatcgc ttcggagacc ccggggaaga acatcttttt ctccccgctg 240
 agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300
 atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360
 ttccagcacc tctgcacac tctcaacctc cccggccatg ggctggaaac acgcgtgggc 420
 agtgctctgt tctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg 480
 gccgtctatg aggctaaact ctccacacc aacttctacg aactgtggg cacaatccag 540
 cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagcgag 600
 ctcaagaagg acgtcttgat ggtgctggtg aattacattt acttcaaagc cctgtgggag 660

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aaaccattca tttcctcaag gaccactccc aaagacttct atgttgatga gaacacaaca 720
gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac 780
ttgccctgct cgggtgctacg gatggattac aaaggagacg caaccgtggt tttcattctc 840
cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattgagg 900
tggaacaact tgttgcggaag gaggaatttt tacaagaagc tagagttgca tcttccaag 960
ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020
ctgtttctcca agtgggctga cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080
aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140
accacgttcg cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200
cggcccttcc ttgtggtgat cttttccacc agcaccaga gtgtcctctt tctgggcaag 1260
gtcgtcgacc ccacgaaacc atag 1284

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<210> 576
<211> 427
<212> PRT
<213> Homo sapiens

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<400> 576

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Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala
1          5          10          15
Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
20          25          30
Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
35          40          45
Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr
50          55          60
Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu
65          70          75          80
Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His
85          90          95
Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu
100         105         110
Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu
115         120         125
Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe
130         135         140

```

Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met
 145 150 155 160
 Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val
 165 170 175
 Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly
 180 185 190
 Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val
 195 200 205
 Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile
 210 215 220
 Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr
 225 230 235 240
 Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu
 245 250 255
 His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly
 260 265 270
 Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu
 275 280 285
 Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu
 290 295 300
 Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys
 305 310 315 320
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
 325 330 335
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
 340 345 350
 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
 355 360 365
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
 370 375 380
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
 385 390 395 400
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
 405 410 415
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
 420 425
 <210> 577
 <211> 1284
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (699)..(699)

<223> wherein N is either a "C" or a "T".

<220>

<221> misc_feature

<222> (1143)..(1143)

<223> wherein N is either a "C" or a "G".

<220>

<221> misc_feature

<222> (412)..(412)

<223> wherein N is either a "C" or a "T".

<220>

<221> misc_feature

<222> (597)..(597)

<223> wherein N is either a "T" or a "C".

<400> 577

atgcatctta tcgactacct gtcctcctg ctggttggac tactggccct ttctcatggc	60
cagctgcacg ttgagcatga tggtagaggt tgcagtaaca gctcccacca gcagattctg	120
gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc	180
cgcttctact acctgatcgc ttcggagacc ccggggaaga acatcttttt ctccccgctg	240
agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag	300
atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc	360
ttccagcacc tcctgcacac tctcaacctc cccggccatg ggctggaaac angcgtgggc	420
agtgctctgt tcctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg	480
gccgtctatg aggctaaact ctccacacc aacttctacg aactgtggg cacaatccag	540
cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagngag	600
ctcaagaagg acgtcttgat ggtgctggtg aattacattt acttcaaagc cctgtgggag	660
aaaccattca tttcctcaag gaccactccc aaagacttnt atgttgatga gaacacaaca	720
gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac	780
ttgccctgct cggtgctacg gatggattac aaaggagacg caaccgtgtt tttcattctc	840
cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattgagg	900

tggaacaact tgttgcgga gaggaat ttt tacaagaagc tagagttgca ttttcccaag 960
 ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020
 ctgttctcca agtgggctga cttatccggc atcaccaaac agcaaaaaact ggaggcatcc 1080
 aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140
 acnacgttcg cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200
 cggcccttcc ttgtggtgat cttttccacc agcaccaga gtgtcctctt tctgggcaag 1260
 gtcgtcgacc ccacgaaacc atag 1284

<210> 578
 <211> 427
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> VARIANT
 <222> (138)..(138)
 <223> wherein Xaa is either "Arg" or a "Cys".

<400> 578

 Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala
 1 5 10 15
 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
 20 25 30
 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
 35 40 45
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr
 50 55 60
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu
 65 70 75 80
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His
 85 90 95
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu
 100 105 110
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu
 115 120 125
 Asn Leu Pro Gly His Gly Leu Glu Thr Xaa Val Gly Ser Ala Leu Phe
 130 135 140
 Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met
 145 150 155 160

Ala	Val	Tyr	Glu	Ala	Lys	Leu	Phe	His	Thr	Asn	Phe	Tyr	Asp	Thr	Val		
				165					170					175			
Gly	Thr	Ile	Gln	Leu	Ile	Asn	Asp	His	Val	Lys	Lys	Glu	Thr	Arg	Gly		
			180					185					190				
Lys	Ile	Val	Asp	Leu	Val	Ser	Glu	Leu	Lys	Lys	Asp	Val	Leu	Met	Val		
		195					200					205					
Leu	Val	Asn	Tyr	Ile	Tyr	Phe	Lys	Ala	Leu	Trp	Glu	Lys	Pro	Phe	Ile		
	210					215					220						
Ser	Ser	Arg	Thr	Thr	Pro	Lys	Asp	Phe	Tyr	Val	Asp	Glu	Asn	Thr	Thr		
225					230					235					240		
Val	Arg	Val	Pro	Met	Met	Leu	Gln	Asp	Gln	Glu	His	His	Trp	Tyr	Leu		
				245					250					255			
His	Asp	Arg	Tyr	Leu	Pro	Cys	Ser	Val	Leu	Arg	Met	Asp	Tyr	Lys	Gly		
			260					265					270				
Asp	Ala	Thr	Val	Phe	Phe	Ile	Leu	Pro	Asn	Gln	Gly	Lys	Met	Arg	Glu		
		275					280					285					
Ile	Glu	Glu	Val	Leu	Thr	Pro	Glu	Met	Leu	Met	Arg	Trp	Asn	Asn	Leu		
	290					295					300						
Leu	Arg	Lys	Arg	Asn	Phe	Tyr	Lys	Lys	Leu	Glu	Leu	His	Leu	Pro	Lys		
305				310						315					320		
Phe	Ser	Ile	Ser	Gly	Ser	Tyr	Val	Leu	Asp	Gln	Ile	Leu	Pro	Arg	Leu		
				325					330				335				
Gly	Phe	Thr	Asp	Leu	Phe	Ser	Lys	Trp	Ala	Asp	Leu	Ser	Gly	Ile	Thr		
			340					345					350				
Lys	Gln	Gln	Lys	Leu	Glu	Ala	Ser	Lys	Ser	Phe	His	Lys	Ala	Thr	Leu		
		355					360					365					
Asp	Val	Asp	Glu	Ala	Gly	Thr	Glu	Ala	Ala	Ala	Ala	Thr	Thr	Phe	Ala		
	370					375						380					
Ile	Lys	Phe	Phe	Ser	Ala	Gln	Thr	Asn	Arg	His	Ile	Leu	Arg	Phe	Asn		
385				390						395					400		
Arg	Pro	Phe	Leu	Val	Val	Ile	Phe	Ser	Thr	Ser	Thr	Gln	Ser	Val	Leu		
				405					410					415			
Phe	Leu	Gly	Lys	Val	Val	Asp	Pro	Thr	Lys	Pro							
			420					425									

<210> 579
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 579
tgtcatcaat ggggtcat 18

<210> 580
<211> 18
<212> DNA
<213> Homo sapiens

<400> 580
cggcggaggc aggcccgg 18

<210> 581
<211> 18
<212> DNA
<213> Homo sapiens

<400> 581
gcctgcatcc tgctcctc 18

<210> 582
<211> 18
<212> DNA
<213> Homo sapiens

<400> 582
acgcgggagg aggtcaga 18

<210> 583
<211> 18
<212> DNA
<213> Homo sapiens

<400> 583
tggagaatgc gtgtattt 18

<210> 584
<211> 18
<212> DNA
<213> Homo sapiens

<400> 584
tgtctgttcg tgaggact 18

<210> 585
<211> 19
<212> DNA
<213> Homo sapiens

<400> 585
ccttccttcc gaagagaac 19

<210> 586
<211> 19
<212> DNA
<213> Homo sapiens

<400> 586
aaacacccgc acccaggaa

19

<210> 587
<211> 19
<212> DNA
<213> Homo sapiens

<400> 587
gtacgtggcg taaaagaa

19

<210> 588
<211> 19
<212> DNA
<213> Homo sapiens

<400> 588
atgacatcat taccagcc

19

<210> 589
<211> 19
<212> DNA
<213> Homo sapiens

<400> 589
catcatcgat gtaatcaca

19

<210> 590
<211> 19
<212> DNA
<213> Homo sapiens

<400> 590
gccagaaagg gggctgcag

19

<210> 591
<211> 19
<212> DNA
<213> Homo sapiens

<400> 591
caggagaact gccatccag

19

<210> 592
<211> 19

<212> DNA
<213> Homo sapiens

<400> 592
aagtgggaac gactgggca 19

<210> 593
<211> 19
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<400> 593
tgaggcatca ttacgcaga 19

<210> 594
<211> 19
<212> DNA
<213> Homo sapiens

<400> 594
aggtgctcat tggctccct 19

<210> 595
<211> 18
<212> DNA
<213> Homo sapiens

<400> 595
tgaaagaacc acatggcc 18

<210> 596
<211> 19
<212> DNA
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<400> 596
atcatagata taaatatat 19

<210> 597
<211> 19
<212> DNA
<213> Homo sapiens

<400> 597
agttgacaac tttcacacc 19

<210> 598
<211> 18
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<400> 598
attagtagcc tacctggt 18

<210> 599
<211> 19
<212> DNA
<213> Homo sapiens

<400> 599
gaatgctaata ataaagata 19

<210> 600
<211> 19
<212> DNA
<213> Homo sapiens

<400> 600
agaataatgc ttggcacac 19

<210> 601
<211> 19
<212> DNA
<213> Homo sapiens

<400> 601
atcagacaca ttttttaggt 19

<210> 602
<211> 19
<212> DNA
<213> Homo sapiens

<400> 602
gcctgcagat gtcctgtac 19

<210> 603
<211> 19
<212> DNA
<213> Homo sapiens

<400> 603
caaagacttc tatgttgat 19

<210> 604
<211> 15
<212> DNA
<213> Homo sapiens

<400> 604
gagttagaac attag 15

<210> 605
<211> 17
<212> DNA
<213> Homo sapiens

<400> 605
cccacaaact gcttcgg 17

<210> 606
<211> 21
<212> DNA
<213> Homo sapiens

<400> 606
cttgagctca ctgaccaaatt c 21

<210> 607
<211> 19
<212> DNA
<213> Homo sapiens

<400> 607
gaggatggct atcctcaga 19

<210> 608
<211> 18
<212> DNA
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<400> 608
tccacaacat ctgtggag 18

<210> 609
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<400> 609
ccaaagttgt ggggatag 18

<210> 610
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<400> 610
tgtttgtttg gttgtttgt 19

<210> 611
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<212> DNA
<213> Homo sapiens

<400> 611
tgatcatcaac ggggtcat 18

<210> 612
<211> 18
<212> DNA
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<210> 801
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<210> 802
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aaaaattagc tgggtgtggc t

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<210> 803
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<210> 814
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<400> 814
ggttgtgctg ctgctattca t

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<210> 815
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tgagggacag ttgcttttca g

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<210> 825
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cctccccat gtctcttat c 21

<210> 826
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<210> 827
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cacactgatt acctcttccg c 21

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<400> 829
actttggatg cctccagttt t 21

<210> 830
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<210> 832
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ccaacagagc aggaaatgaa g 21

<210> 833
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<400> 833
 taagtgcacct gcccaaagtt g

21

<210> 834
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<400> 834
 taagtgcacct gcccaaagtt g

21

<210> 835
 <211> 353
 <212> PRT
 <213> Mus musculus

<400> 835

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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
 20 25 30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
 130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg

165	170	175
Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu 180 185 190		
Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile 195 200 205		
Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His 210 215 220		
Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val 225 230 235 240		
Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val 245 250 255		
Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu 260 265 270		
Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp 275 280 285		
Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn 290 295 300		
Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg 305 310 315 320		
Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala 325 330 335		
Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg 340 345 350		

Asn

<210> 836
 <211> 352
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 836

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Asp Leu Leu His Arg Leu Leu Pro Thr Phe Ile Ile Ala Ile Phe Thr 35 40 45
Leu Gly Leu Leu Gly Asn Ser Phe Val Leu Ser Val Phe Leu Leu Ala 50 55 60

Arg Arg Arg Leu Ser Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala Ala
 65 70 75 80
 Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn Val
 85 90 95
 Arg Asn Gln Phe Asp Trp Pro Phe Gly Ala Ala Leu Cys Arg Ile Val
 100 105 110
 Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val Val
 115 120 125
 Ala Ile Ser Gln Asp Arg Tyr Ser Val Leu Val His Pro Met Ala Ser
 130 135 140
 Arg Arg Gly Arg Arg Arg Arg Gln Ala Gln Ala Thr Cys Ala Leu Ile
 145 150 155 160
 Trp Leu Ala Gly Gly Leu Leu Ser Thr Pro Thr Phe Val Leu Arg Ser
 165 170 175
 Val Arg Ala Val Pro Glu Leu Asn Val Ser Ala Cys Ile Leu Leu Leu
 180 185 190
 Pro His Glu Ala Trp His Trp Leu Arg Met Val Glu Leu Asn Leu Leu
 195 200 205
 Gly Phe Leu Leu Pro Leu Ala Ala Ile Leu Phe Phe Asn Cys His Ile
 210 215 220
 Leu Ala Ser Leu Arg Arg Arg Gly Glu Arg Val Pro Ser Arg Cys Gly
 225 230 235 240
 Gly Pro Arg Asp Ser Lys Ser Thr Ala Leu Ile Leu Thr Leu Val Ala
 245 250 255
 Ser Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu Glu
 260 265 270
 Cys Leu Trp Gln Val His Ala Ile Gly Gly Cys Phe Trp Glu Glu Phe
 275 280 285
 Thr Asp Leu Gly Leu Gln Leu Ser Asn Phe Ser Ala Phe Val Asn Ser
 290 295 300
 Cys Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg Thr
 305 310 315 320
 Lys Val Trp Glu Leu Cys Gln Gln Cys Ser Pro Arg Ser Leu Ala Pro
 325 330 335
 Val Ser Ser Ser Arg Arg Lys Glu Met Leu Trp Gly Phe Trp Arg Asn
 340 345 350
 <210> 837
 <211> 337
 <212> PRT

<213> Rattus norvegicus

<400> 837

Met Ala Ser Glu Val Leu Leu Glu Leu Gln Pro Ser Asn Arg Ser Leu
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Gln Ala Pro Ala Asn Ile Thr Ser Cys Glu Ser Ala Leu Glu Asp Trp
20 25 30
Asp Leu Leu Tyr Arg Val Leu Pro Gly Phe Val Ile Thr Ile Cys Phe
35 40 45
Phe Gly Leu Leu Gly Asn Leu Leu Val Leu Ser Phe Phe Leu Leu Pro
50 55 60
Trp Arg Gln Trp Trp Trp Gln Gln Arg Gln Arg Gln Gln Arg Leu Thr
65 70 75 80
Ile Ala Glu Ile Tyr Leu Ala Asn Leu Ala Ala Ser Asp Leu Val Phe
85 90 95
Val Leu Gly Leu Pro Phe Trp Ala Glu Asn Ile Gly Asn Arg Phe Asn
100 105 110
Trp Pro Phe Gly Thr Asp Leu Cys Arg Val Val Ser Gly Val Ile Lys
115 120 125
Ala Asn Leu Phe Val Ser Ile Phe Leu Val Val Ala Ile Ser Gln Asp
130 135 140
Arg Tyr Arg Leu Leu Val Tyr Pro Met Thr Ser Trp Gly Tyr Arg Arg
145 150 155 160
Arg Arg Gln Ala Gln Ala Thr Cys Leu Leu Ile Trp Val Ala Gly Gly
165 170 175
Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg Ser Val Lys Val Val Pro
180 185 190
Asp Leu Asn Val Ser Ala Cys Ile Leu Leu Phe Pro His Glu Ala Trp
195 200 205
His Phe Ala Arg Met Val Glu Leu Asn Val Leu Gly Phe Leu Leu Pro
210 215 220
Val Thr Ala Ile Ile Phe Phe Asn Tyr His Ile Leu Ala Ser Leu Arg
225 230 235 240
Gly Gln Lys Glu Ala Ser Arg Thr Arg Cys Gly Gly Pro Lys Gly Ser
245 250 255
Lys Thr Thr Gly Leu Ile Leu Thr Leu Val Ala Ser Phe Leu Val Cys
260 265 270
Trp Cys Pro Tyr His Phe Phe Ala Phe Leu Asp Phe Leu Val Gln Val
275 280 285

Arg Val Ile Gln Asp Cys Ser Trp Lys Glu Ile Thr Asp Leu Gly Leu
 290 295 300

Gln Leu Ala Asn Phe Phe Ala Phe Val Asn Ser Cys Leu Asn Pro Leu
 305 310 315 320

Ile Tyr Val Phe Ala Gly Arg Leu Leu Lys Thr Arg Val Leu Gly Thr
 325 330 335

Leu

<210> 838

<211> 392

<212> PRT

<213> Mus musculus

<400> 838

Met Pro Cys Ser Trp Lys Leu Leu Gly Phe Leu Ser Val His Glu Pro
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Met Pro Thr Ala Ala Ser Phe Gly Ile Glu Met Phe Asn Val Thr Thr
 20 25 30

Gln Val Leu Gly Ser Ala Leu Asn Gly Thr Leu Ser Lys Asp Asn Cys
 35 40 45

Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile Gln Ala Pro Phe
 50 55 60

Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn Leu Phe Val Leu
 65 70 75 80

Ser Val Phe Phe Leu His Lys Asn Ser Cys Thr Val Ala Glu Ile Tyr
 85 90 95

Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro
 100 105 110

Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp Val Phe Gly Glu
 115 120 125

Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met Asn Leu Tyr Ser
 130 135 140

Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu
 145 150 155 160

Val Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys
 165 170 175

Leu Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro
 180 185 190

Met Leu Val Phe Arg Thr Met Arg Glu Tyr Ser Glu Glu Gly His Asn

195	200	205
Val Thr Ala Cys Val Ile Val Tyr Pro Ser Arg Ser Trp Glu Val Phe		
210	215	220
Thr Asn Val Leu Leu Asn Leu Val Gly Phe Leu Leu Pro Leu Ser Val		
225	230	235
Ile Thr Phe Cys Thr Val Arg Ile Leu Gln Val Leu Arg Asn Asn Glu		
	245	250
Met Lys Lys Phe Lys Glu Val Gln Thr Glu Arg Lys Ala Thr Val Leu		
	260	270
Val Leu Ala Val Leu Gly Leu Phe Val Leu Cys Trp Val Pro Phe Gln		
	275	285
Ile Ser Thr Phe Leu Asp Thr Leu Leu Arg Leu Gly Val Leu Ser Gly		
	290	300
Cys Trp Asp Glu His Ala Val Asp Val Ile Thr Gln Ile Ser Ser Tyr		
305	310	315
Val Ala Tyr Ser Asn Ser Gly Leu Asn Pro Leu Val Tyr Val Ile Val		
	325	330
Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr Arg Val Leu Cys		
	340	345
Gln Lys Gly Gly Cys Met Gly Glu Pro Val Gln Met Glu Asn Ser Met		
	355	360
Gly Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu		
	370	375
Gln Asp Trp Ala Gly Lys Lys Gln		
385	390	

<210> 839
 <211> 367
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 839

Met Leu Asn Ile Thr Ser Gln Val Leu Ala Pro Ala Leu Asn Gly Ser
1 5 10 15
Val Ser Gln Ser Ser Gly Cys Pro Asn Thr Glu Trp Ser Gly Trp Leu
20 25 30
Asn Val Ile Gln Ala Pro Phe Leu Trp Val Leu Phe Val Leu Ala Thr
35 40 45
Leu Glu Asn Leu Phe Val Leu Ser Val Phe Cys Leu His Lys Ser Ser
50 55 60

Cys Thr Val Ala Glu Val Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu
 65 70 75 80
 Ile Leu Ala Cys Gly Leu Pro Phe Trp Ala Val Thr Ile Ala Asn His
 85 90 95
 Phe Asp Trp Leu Phe Gly Glu Ala Leu Cys Arg Val Val Asn Thr Met
 100 105 110
 Ile Tyr Met Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser
 115 120 125
 Ile Asp Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Ile Gly Arg Met
 130 135 140
 Arg Arg Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys
 145 150 155 160
 Thr Leu Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp
 165 170 175
 Tyr Arg Asp Glu Gly Tyr Asn Val Thr Ala Cys Ile Ile Asp Tyr Pro
 180 185 190
 Ser Arg Ser Trp Glu Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly
 195 200 205
 Phe Leu Leu Pro Leu Ser Val Ile Thr Phe Cys Thr Val Gln Ile Leu
 210 215 220
 Gln Val Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr
 225 230 235 240
 Glu Arg Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Leu Phe Val
 245 250 255
 Val Cys Trp Leu Pro Phe Gln Val Ser Thr Phe Leu Asp Thr Leu Leu
 260 265 270
 Lys Leu Gly Val Leu Ser Ser Cys Trp Asp Glu His Val Ile Asp Val
 275 280 285
 Ile Thr Gln Val Gly Ser Phe Met Gly Tyr Ser Asn Ser Cys Leu Asn
 290 295 300
 Pro Leu Val Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg
 305 310 315 320
 Glu Val Tyr Arg Ala Ala Cys Pro Lys Ala Gly Cys Val Leu Glu Pro
 325 330 335
 Val Gln Ala Glu Ser Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val
 340 345 350
 Glu Arg Gln Ile His Lys Leu Pro Glu Trp Thr Arg Ser Ser Gln
 355 360 365

<210> 840
 <211> 372
 <212> PRT
 <213> Cavia porcellus

<400> 840

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Met Phe Asn Ile Thr Ser Gln Val Ser Ala Leu Asn Ala Thr Leu Ala
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Gln Gly Asn Ser Cys Leu Asp Ala Glu Trp Trp Ser Trp Leu Asn Thr
          20           25           30

Ile Gln Ala Pro Phe Leu Trp Val Leu Phe Val Leu Ala Val Leu Glu
          35           40           45

Asn Ile Phe Val Leu Ser Val Phe Phe Leu His Lys Ser Ser Cys Thr
          50           55           60

Val Ala Glu Ile Tyr Leu Gly Asn Leu Ala Val Ala Asp Leu Ile Leu
65           70           75           80

Ala Phe Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp
          85           90           95

Trp Leu Phe Gly Glu Val Leu Cys Arg Met Val Asn Thr Met Ile Gln
          100          105          110

Met Asn Met Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp
          115          120          125

Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Met Gly Arg Met Arg Gly
          130          135          140

Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys Ala Leu
145          150          155          160

Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp Tyr Arg
          165          170          175

Asp Glu Gly His Asn Val Thr Ala Cys Leu Ile Ile Tyr Pro Ser Leu
          180          185          190

Thr Trp Gln Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly Phe Leu
          195          200          205

Leu Pro Leu Ser Ile Ile Thr Phe Cys Thr Val Gln Ile Met Gln Val
          210          215          220

Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg
225          230          235          240

Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Leu Phe Val Val Cys
          245          250          255

Trp Leu Pro Phe Gln Ile Gly Thr Phe Leu Asp Thr Leu Arg Leu Leu
          260          265          270

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Gly Phe Leu Pro Gly Cys Trp Glu His Val Ile Asp Leu Ile Thr Gln
 275 280 285

Ile Ser Ser Tyr Leu Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val
 290 295 300

Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr
 305 310 315 320

His Gly Leu Cys Arg Ser Gly Gly Cys Val Ser Glu Pro Ala Gln Ser
 325 330 335

Glu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln
 340 345 350

Ile His Lys Leu Gln Asp Trp Ala Arg Ser Ser Ser Glu Gly Thr Pro
 355 360 365

Pro Gly Leu Leu
 370

<210> 841
 <211> 396
 <212> PRT
 <213> Rattus norvegicus

<400> 841

Met Asp Thr Arg Ser Ser Leu Cys Pro Lys Thr Gln Ala Val Val Ala
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Val Phe Trp Gly Pro Gly Cys His Leu Ser Thr Cys Ile Glu Met Phe
 20 25 30

Asn Ile Thr Thr Gln Ala Leu Gly Ser Ala His Asn Gly Thr Phe Ser
 35 40 45

Glu Val Asn Cys Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile
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Gln Ala Pro Phe Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn
 65 70 75 80

Ile Phe Val Leu Ser Val Phe Cys Leu His Lys Thr Asn Cys Thr Val
 85 90 95

Ala Glu Ile Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala
 100 105 110

Cys Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp
 115 120 125

Leu Phe Gly Glu Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met
 130 135 140

Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg

145		150		155		160									
Tyr	Leu	Ala	Leu	Val	Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	Val
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Arg	Trp	Ala	Lys	Leu	Tyr	Ser	Leu	Val	Ile	Trp	Ser	Cys	Thr	Leu	Leu
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Trp	Glu	Val	Phe	Thr	Asn	Met	Leu	Leu	Asn	Leu	Val	Gly	Phe	Leu	Leu
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Pro	Leu	Ser	Ile	Ile	Thr	Phe	Cys	Thr	Val	Arg	Ile	Met	Gln	Val	Leu
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Arg	Asn	Asn	Glu	Met	Lys	Lys	Phe	Lys	Glu	Val	Gln	Thr	Glu	Lys	Lys
			260					265					270		
Ala	Thr	Val	Leu	Val	Leu	Ala	Val	Leu	Gly	Leu	Phe	Val	Leu	Cys	Trp
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		290				295					300				
Val	Leu	Ser	Gly	Cys	Trp	Asn	Glu	Arg	Ala	Val	Asp	Ile	Val	Thr	Gln
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Ile	Ser	Ser	Tyr	Val	Ala	Tyr	Ser	Asn	Ser	Cys	Leu	Asn	Pro	Leu	Val
			325						330					335	
Tyr	Val	Ile	Val	Gly	Lys	Arg	Phe	Arg	Lys	Lys	Ser	Arg	Glu	Val	Tyr
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Gln	Ala	Ile	Cys	Arg	Lys	Gly	Gly	Cys	Met	Gly	Glu	Ser	Val	Gln	Met
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Glu	Asn	Ser	Met	Gly	Thr	Leu	Arg	Thr	Ser	Ile	Ser	Val	Asp	Arg	Gln
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<210> 842
 <211> 3405
 <212> DNA
 <213> homo sapiens

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 <222> (2173)..(2173)
 <223> wherein N is either a "T" or a "C".

<400> 842

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agaaattcag aatctcacag tcaagcttca gctgcaggct cttcagcaaa atgggtcttc	420
agtgtcttca gaagacaaga gcaaacgggt gaacacaatt ctaaatacaa tgagcaccat	480
ctacagtact ggaaaagttt gtaaccacaga taatccacaa gaatgcttat tacttgaacc	540
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aagctggaga tctgaggtcg gcaagcagct gaggccatta tatgaagagt atgtgggtctt	660
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ggaacatacc tttgaagaga ttaaaccatt atatgaacat cttcatgcct atgtgagggc	840
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tgcacaacct tttctgctaa gaaatggagc taatgaagga ttccatgaag ctgttgggga	1320
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tgttgggact ctgccattta cttacatgtt agagaagtgg aggtggatgg tctttaaggg	1500
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3405

<210> 843
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<213> homo sapiens

<400> 843

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Ala	Gln	Ser	Thr	Ile	Glu	Glu	Gln	Ala	Lys	Thr	Phe	Leu	Asp	Lys	Phe	
			20					25					30			
Asn	His	Glu	Ala	Glu	Asp	Leu	Phe	Tyr	Gln	Ser	Ser	Leu	Ala	Ser	Trp	
		35					40					45				
Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Val	Gln	Asn	Met	Asn	Asn	
	50					55					60					
Ala	Gly	Asp	Lys	Trp	Ser	Ala	Phe	Leu	Lys	Glu	Gln	Ser	Thr	Leu	Ala	
65					70					75					80	
Gln	Met	Tyr	Pro	Leu	Gln	Glu	Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln	
				85					90					95		
Leu	Gln	Ala	Leu	Gln	Gln	Asn	Gly	Ser	Ser	Val	Leu	Ser	Glu	Asp	Lys	
			100					105					110			
Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser	
		115					120						125			
Thr	Gly	Lys	Val	Cys	Asn	Pro	Asp	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu	
	130					135					140					
Glu	Pro	Gly	Leu	Asn	Glu	Ile	Met	Ala	Asn	Ser	Leu	Asp	Tyr	Asn	Glu	
145					150					155					160	
Arg	Leu	Trp	Ala	Trp	Glu	Ser	Trp	Arg	Ser	Glu	Val	Gly	Lys	Gln	Leu	
				165					170					175		
Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg	
			180					185					190			
Ala	Asn	His	Tyr	Glu	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu	
		195					200					205				
Val	Asn	Gly	Val	Asp	Gly	Tyr	Asp	Tyr	Ser	Arg	Gly	Gln	Leu	Ile	Glu	
	210					215					220					
Asp	Val	Glu	His	Thr	Phe	Glu	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu	
225					230					235					240	
His	Ala	Tyr	Val	Arg	Ala	Lys	Leu	Met	Asn	Ala	Tyr	Pro	Ser	Tyr	Ile	
				245					250					255		

Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
 260 265 270
 Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys
 275 280 285
 Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala
 290 295 300
 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
 305 310 315 320
 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
 325 330 335
 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
 340 345 350
 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
 355 360 365
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
 370 375 380
 Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
 385 390 395 400
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
 405 410 415
 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn
 420 425 430
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
 435 440 445
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
 450 455 460
 Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met
 465 470 475 480
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
 500 505 510
 Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala
 515 520 525
 Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile
 530 535 540
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu
 545 550 555 560

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Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala
565 570 575
Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe
580 585 590
Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr
595 600 605
Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
610 615 620
Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met
625 630 635 640
Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu
645 650 655
Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val
660 665 670
Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro
675 680 685
Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
690 695 700
Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
705 710 715 720
Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln
725 730 735
Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
740 745 750
Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
755 760 765
Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile
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Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp
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Val Gln Thr Ser Phe
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<210> 844
<211> 3733
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (40)..(40)

<223> wherein N is either a "C" or a "T".

<220>

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<222> (47)..(47)

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<222> (933)..(933)

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<222> (1061)..(1061)

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<400> 844

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gcctacagca acagctgct caaccactg gtgtacgtga tcgtgggcaa gcgcttccga	1020
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aaaaaaaaaa aaa 3733

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<210> 845
<211> 391
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (14)..(14)
<223> wherein Xaa is either "Arg" or a "Cys".

<220>
<221> VARIANT
<222> (16)..(16)
<223> wherein Xaa is either "Asp" or a "Ala".

<220>
<221> VARIANT
<222> (354)..(354)
<223> wherein Xaa is either "Gly" or a "Glu".

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<400> 845

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Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr
20 25 30
Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro
35 40 45
Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
50 55 60
Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
65 70 75 80
Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
85 90 95
Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
100 105 110
Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125
Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser
130 135 140
Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val
145 150 155 160
Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu
165 170 175
Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met
180 185 190
Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val
195 200 205
Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr
210 215 220
Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile
225 230 235 240
Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met
245 250 255
Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val
260 265 270
Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile
275 280 285

Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
 290 295 300

Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
 305 310 315 320

Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
 325 330 335

Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
 340 345 350

Lys Xaa Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly
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Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln
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Asp Trp Ala Gly Ser Arg Gln
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<210> 846
 <211> 3428
 <212> DNA
 <213> homo sapiens

<400> 846
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<210> 847
<211> 673
<212> PRT
<213> homo sapiens

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<400> 847

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20         25         30
Val Arg Asn Cys Ser Thr Asn Pro Pro Tyr Leu Pro Val Thr Val Val
35         40         45
Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln
50         55         60
Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu
65         70         75         80
Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr
85         90         95
Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp
100        105        110

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Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser
 420 425 430
 Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu
 435 440 445
 Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg
 450 455 460
 Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr
 465 470 475 480
 Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala
 485 490 495
 Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp
 500 505 510
 Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn
 515 520 525
 Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile
 530 535 540
 Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys
 545 550 555 560
 Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu
 565 570 575
 Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe
 580 585 590
 Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu
 595 600 605
 His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val
 610 615 620
 Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu
 625 630 635 640
 Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser
 645 650 655
 Trp Ala Ser Val Leu Val Val Ser Thr Leu Ala Ile Leu Gly Trp Ser
 660 665 670

Val

<210> 848
 <211> 1082
 <212> DNA
 <213> homo sapiens

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Ala	Ser	Asp	Leu	Val	Phe	Val	Leu	Gly	Leu	Pro	Phe	Trp	Ala	Glu	Asn
				85					90					95	
Ile	Trp	Asn	Gln	Phe	Asn	Trp	Pro	Phe	Gly	Ala	Leu	Leu	Cys	Arg	Val
			100						105					110	
Ile	Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val
		115					120					125			
Val	Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Arg	Val	Leu	Val	His	Pro	Met	Ala
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Ser	Gly	Arg	Gln	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Val	Thr	Cys	Val	Leu
145						150					155				160
Ile	Trp	Val	Val	Gly	Gly	Leu	Leu	Ser	Ile	Pro	Thr	Phe	Leu	Leu	Arg
				165					170						175
Ser	Ile	Gln	Ala	Val	Pro	Asp	Leu	Asn	Ile	Thr	Ala	Cys	Ile	Leu	Leu
			180					185					190		
Leu	Pro	His	Glu	Ala	Trp	His	Phe	Ala	Arg	Ile	Val	Glu	Leu	Asn	Ile
		195					200					205			
Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Ile	Val	Phe	Phe	Asn	Tyr	His
	210					215					220				
Ile	Leu	Ala	Ser	Leu	Arg	Thr	Arg	Glu	Glu	Val	Ser	Arg	Thr	Arg	Val
225						230					235				240
Gln	Gly	Pro	Lys	Asp	Ser	Lys	Thr	Thr	Ala	Leu	Ile	Leu	Thr	Leu	Val
				245					250					255	
Val	Ala	Phe	Leu	Val	Cys	Trp	Ala	Pro	Tyr	His	Phe	Phe	Ala	Phe	Leu
			260					265					270		
Glu	Phe	Leu	Phe	Gln	Val	Gln	Ala	Val	Arg	Gly	Cys	Phe	Trp	Glu	Asp
		275					280					285			
Phe	Ile	Asp	Leu	Gly	Leu	Gln	Leu	Ala	Asn	Phe	Phe	Ala	Phe	Thr	Asn
	290					295					300				
Ser	Ser	Leu	Asn	Pro	Val	Ile	Tyr	Val	Phe	Val	Gly	Arg	Leu	Phe	Arg
305						310					315				320
Thr	Lys	Val	Trp	Glu	Leu	Tyr	Lys	Gln	Cys	Thr	Pro	Lys	Ser	Leu	Ala
				325					330					335	
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Asn

<210> 850
 <211> 3733
 <212> DNA
 <213> homo sapiens

<400> 850
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<210> 851
<211> 391
<212> PRT
<213> homo sapiens

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<400> 851

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Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr
          20          25          30
Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro
          35          40          45
Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
50          55          60
Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
65          70          75          80
Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
          85          90          95
Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
100          105          110
Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115          120          125
Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser
130          135          140
Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val
145          150          155          160

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<210> 853
 <211> 427
 <212> PRT
 <213> homo sapiens
 <400> 853

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 20 25 30
 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
 35 40 45
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr

50					55					60					
Leu	Ile	Ala	Ser	Glu	Thr	Pro	Gly	Lys	Asn	Ile	Phe	Phe	Ser	Pro	Leu
65					70					75					80
Ser	Ile	Ser	Ala	Ala	Tyr	Ala	Met	Leu	Ser	Leu	Gly	Ala	Cys	Ser	His
				85					90					95	
Ser	Arg	Ser	Gln	Ile	Leu	Glu	Gly	Leu	Gly	Phe	Asn	Leu	Thr	Glu	Leu
			100					105					110		
Ser	Glu	Ser	Asp	Val	His	Arg	Gly	Phe	Gln	His	Leu	Leu	His	Thr	Leu
			115				120					125			
Asn	Leu	Pro	Gly	His	Gly	Leu	Glu	Thr	Arg	Val	Gly	Ser	Ala	Leu	Phe
	130					135					140				
Leu	Ser	His	Asn	Leu	Lys	Phe	Leu	Ala	Lys	Phe	Leu	Asn	Asp	Thr	Met
145					150					155					160
Ala	Val	Tyr	Glu	Ala	Lys	Leu	Phe	His	Thr	Asn	Phe	Tyr	Asp	Thr	Val
				165					170					175	
Gly	Thr	Ile	Gln	Leu	Ile	Asn	Asp	His	Val	Lys	Lys	Glu	Thr	Arg	Gly
			180					185					190		
Lys	Ile	Val	Asp	Leu	Val	Ser	Glu	Leu	Lys	Lys	Asp	Val	Leu	Met	Val
			195				200					205			
Leu	Val	Asn	Tyr	Ile	Tyr	Phe	Lys	Ala	Leu	Trp	Glu	Lys	Pro	Phe	Ile
	210					215					220				
Ser	Ser	Arg	Thr	Thr	Pro	Lys	Asp	Phe	Tyr	Val	Asp	Glu	Asn	Thr	Thr
225					230					235					240
Val	Arg	Val	Pro	Met	Met	Leu	Gln	Asp	Gln	Glu	His	His	Trp	Tyr	Leu
				245					250					255	
His	Asp	Arg	Tyr	Leu	Pro	Cys	Ser	Val	Leu	Arg	Met	Asp	Tyr	Lys	Gly
			260					265					270		
Asp	Ala	Thr	Val	Phe	Phe	Ile	Leu	Pro	Asn	Gln	Gly	Lys	Met	Arg	Glu
		275					280					285			
Ile	Glu	Glu	Val	Leu	Thr	Pro	Glu	Met	Leu	Met	Arg	Trp	Asn	Asn	Leu
	290					295					300				
Leu	Arg	Lys	Arg	Asn	Phe	Tyr	Lys	Lys	Leu	Glu	Leu	His	Leu	Pro	Lys
305				310						315					320
Phe	Ser	Ile	Ser	Gly	Ser	Tyr	Val	Leu	Asp	Gln	Ile	Leu	Pro	Arg	Leu
				325					330					335	
Gly	Phe	Thr	Asp	Leu	Phe	Ser	Lys	Trp	Ala	Asp	Leu	Ser	Gly	Ile	Thr
			340					345					350		
Lys	Gln	Gln	Lys	Leu	Glu	Ala	Ser	Lys	Ser	Phe	His	Lys	Ala	Thr	Leu

accacgttcg cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200
 cggcccttcc ttgtggtgat cttttccacc agcaccaga gtgtcctctt tctgggcaag 1260
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<210> 855
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 <212> PRT
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<400> 855

Met	His	Leu	Ile	Asp	Tyr	Leu	Leu	Leu	Leu	Leu	Val	Gly	Leu	Leu	Ala	1	5	10	15
Leu	Ser	His	Gly	Gln	Leu	His	Val	Glu	His	Asp	Gly	Glu	Ser	Cys	Ser	20	25	30	
Asn	Ser	Ser	His	Gln	Gln	Ile	Leu	Glu	Thr	Gly	Glu	Gly	Ser	Pro	Ser	35	40	45	
Leu	Lys	Ile	Ala	Pro	Ala	Asn	Ala	Asp	Phe	Ala	Phe	Arg	Phe	Tyr	Tyr	50	55	60	
Leu	Ile	Ala	Ser	Glu	Thr	Pro	Gly	Lys	Asn	Ile	Phe	Phe	Ser	Pro	Leu	65	70	75	80
Ser	Ile	Ser	Ala	Ala	Tyr	Ala	Met	Leu	Ser	Leu	Gly	Ala	Cys	Ser	His	85	90	95	
Ser	Arg	Ser	Gln	Ile	Leu	Glu	Gly	Leu	Gly	Phe	Asn	Leu	Thr	Glu	Leu	100	105	110	
Ser	Glu	Ser	Asp	Val	His	Arg	Gly	Phe	Gln	His	Leu	Leu	His	Thr	Leu	115	120	125	
Asn	Leu	Pro	Gly	His	Gly	Leu	Glu	Thr	Cys	Val	Gly	Ser	Ala	Leu	Phe	130	135	140	
Leu	Ser	His	Asn	Leu	Lys	Phe	Leu	Ala	Lys	Phe	Leu	Asn	Asp	Thr	Met	145	150	155	160
Ala	Val	Tyr	Glu	Ala	Lys	Leu	Phe	His	Thr	Asn	Phe	Tyr	Asp	Thr	Val	165	170	175	
Gly	Thr	Ile	Gln	Leu	Ile	Asn	Asp	His	Val	Lys	Lys	Glu	Thr	Arg	Gly	180	185	190	
Lys	Ile	Val	Asp	Leu	Val	Ser	Glu	Leu	Lys	Lys	Asp	Val	Leu	Met	Val	195	200	205	
Leu	Val	Asn	Tyr	Ile	Tyr	Phe	Lys	Ala	Leu	Trp	Glu	Lys	Pro	Phe	Ile	210	215	220	

Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr
 225 230 235 240
 Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu
 245 250 255
 His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly
 260 265 270
 Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu
 275 280 285
 Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu
 290 295 300
 Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys
 305 310 315 320
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
 325 330 335
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
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 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
 355 360 365
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
 370 375 380
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
 385 390 395 400
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
 405 410 415
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
 420 425

<210> 856
 <211> 3428
 <212> DNA
 <213> homo sapiens

<220>
 <221> misc_feature
 <222> (711)..(711)
 <223> wherein N is either an "T" or a "C".

<220>
 <221> misc_feature
 <222> (2085)..(2085)
 <223> wherein N is either an "C" or a "G".

<400> 856

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 gcagccaaac gcctccttct tgacgccagc cccaccctc tgtctgctcg agcccaggaa 180
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 ccagcgccgg catctggaga ccctatggcc cgggctcact ggggctgctg ccctggctg 300
 gtccctcctct gtgcttgctg ctggggccac acaaagccac tggaccttgg agggcaggat 360
 gtgagaaatt gttccacca ccccccttac cttccagtta ctgtggtcaa taccacaatg 420
 tctctcacag cctccgccca gcagatgcag acccagaatc tctcagccta catcatccca 480
 ggcacagatg ctccatgaa cgagtacatc ggccaacatg acgagaggcg tgcgtggatt 540
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 accgacagtc gctaactggac tcaggctgag cggcaaattg actgtaattg ggagctccat 660
 aaggaagttg gcaccactcc tattgtcacc tggctcctca ccgagattcc ngctggaggg 720
 cgtgtggggt ttgaccctt cctcttgctc attgacacct gggagagtta tgatctggcc 780
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3428

<210> 857
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<400> 857

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Ala	Cys	Ala	Trp	Gly	His	Thr	Lys	Pro	Leu	Asp	Leu	Gly	Gly	Gln	Asp
			20					25					30		
Val	Arg	Asn	Cys	Ser	Thr	Asn	Pro	Pro	Tyr	Leu	Pro	Val	Thr	Val	Val
		35					40					45			
Asn	Thr	Thr	Met	Ser	Leu	Thr	Ala	Leu	Arg	Gln	Gln	Met	Gln	Thr	Gln
		50				55					60				
Asn	Leu	Ser	Ala	Tyr	Ile	Ile	Pro	Gly	Thr	Asp	Ala	His	Met	Asn	Glu
65					70					75					80
Tyr	Ile	Gly	Gln	His	Asp	Glu	Arg	Arg	Ala	Trp	Ile	Thr	Gly	Phe	Thr
				85					90					95	
Gly	Ser	Ala	Gly	Thr	Ala	Val	Val	Thr	Met	Lys	Lys	Ala	Ala	Val	Trp
			100					105					110		
Thr	Asp	Ser	Arg	Tyr	Trp	Thr	Gln	Ala	Glu	Arg	Gln	Met	Asp	Cys	Asn
		115					120					125			
Trp	Glu	Leu	His	Lys	Glu	Val	Gly	Thr	Thr	Pro	Ile	Val	Thr	Trp	Leu
		130				135					140				
Leu	Thr	Glu	Ile	Pro	Ala	Gly	Gly	Arg	Val	Gly	Phe	Asp	Pro	Phe	Leu
145					150					155					160
Leu	Ser	Ile	Asp	Thr	Trp	Glu	Ser	Tyr	Asp	Leu	Ala	Leu	Gln	Gly	Ser
			165						170					175	
Asn	Arg	Gln	Leu	Val	Ser	Ile	Thr	Thr	Asn	Leu	Val	Asp	Leu	Val	Trp
			180					185					190		
Gly	Ser	Glu	Arg	Pro	Pro	Val	Pro	Asn	Gln	Pro	Ile	Tyr	Ala	Leu	Gln
		195					200					205			
Glu	Ala	Phe	Thr	Gly	Ser	Thr	Trp	Gln	Glu	Lys	Val	Ser	Gly	Val	Arg
		210				215					220				
Ser	Gln	Met	Gln	Lys	His	Gln	Lys	Val	Pro	Thr	Ala	Val	Leu	Leu	Ser
225					230					235					240
Ala	Leu	Glu	Glu	Thr	Ala	Trp	Leu	Phe	Asn	Leu	Arg	Ala	Ser	Asp	Ile
				245					250					255	

Pro	Tyr	Asn	Pro	Phe	Phe	Tyr	Ser	Tyr	Thr	Leu	Leu	Thr	Asp	Ser	Ser		
			260					265					270				
Ile	Arg	Leu	Phe	Ala	Asn	Lys	Ser	Arg	Phe	Ser	Ser	Glu	Thr	Leu	Ser		
		275					280					285					
Tyr	Leu	Asn	Ser	Ser	Cys	Thr	Gly	Pro	Met	Cys	Val	Gln	Ile	Glu	Asp		
	290					295					300						
Tyr	Ser	Gln	Val	Arg	Asp	Ser	Ile	Gln	Ala	Tyr	Ser	Leu	Gly	Asp	Val		
305					310					315					320		
Arg	Ile	Trp	Ile	Gly	Thr	Ser	Tyr	Thr	Met	Tyr	Gly	Ile	Tyr	Glu	Met		
				325					330					335			
Ile	Pro	Arg	Glu	Lys	Leu	Val	Thr	Asp	Thr	Tyr	Ser	Pro	Val	Met	Met		
			340					345					350				
Thr	Lys	Ala	Val	Lys	Asn	Ser	Lys	Glu	Gln	Ala	Leu	Leu	Lys	Ala	Ser		
		355					360					365					
His	Val	Arg	Asp	Ala	Val	Ala	Val	Ile	Arg	Tyr	Leu	Val	Trp	Leu	Glu		
	370					375					380						
Lys	Asn	Val	Pro	Lys	Gly	Thr	Val	Asp	Glu	Phe	Ser	Gly	Ala	Glu	Ile		
385					390					395					400		
Val	Asp	Lys	Phe	Arg	Gly	Glu	Glu	Gln	Phe	Ser	Ser	Gly	Pro	Ser	Phe		
				405					410					415			
Glu	Thr	Ile	Ser	Ala	Ser	Gly	Leu	Asn	Ala	Ala	Leu	Ala	His	Tyr	Ser		
			420					425					430				
Pro	Thr	Lys	Glu	Leu	Asn	Arg	Lys	Leu	Ser	Ser	Asp	Glu	Met	Tyr	Leu		
		435					440					445					
Leu	Asp	Ser	Gly	Gly	Gln	Tyr	Trp	Asp	Gly	Thr	Thr	Asp	Ile	Thr	Arg		
	450					455					460						
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465					470					475					480		
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				485				490						495			
Ala	Thr	Ser	Gly	Arg	Met	Val	Glu	Ala	Phe	Ala	Arg	Arg	Ala	Leu	Trp		
			500					505					510				
Asp	Ala	Gly	Leu	Asn	Tyr	Gly	His	Gly	Thr	Gly	His	Gly	Ile	Gly	Asn		
		515					520					525					
Phe	Leu	Cys	Val	His	Glu	Trp	Pro	Val	Gly	Phe	Gln	Ser	Asn	Asn	Ile		
	530					535					540						
Ala	Met	Ala	Lys	Gly	Met	Phe	Thr	Ser	Ile	Glu	Pro	Gly	Tyr	Tyr	Lys		
545					550					555					560		

Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu
565 570 575

Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe
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Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu
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His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val
610 615 620

Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu
625 630 635 640

Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser
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Trp Ala Ser Val Leu Val Val Ser Thr Leu Ala Ile Leu Gly Trp Ser
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catcttgaag gaactcaaag actca	25
<210> 1201	
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<400> 1201	
ctttggatga aaaagaggaa gca	23
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<400> 1202	
caagagaagg cgtcttttga t	21
<210> 1203	
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<213> Homo sapiens	

<400> 1203 caaagaggcc ctgcccga	18
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<400> 1204 aaccoccttac ccaccagc	18
<210> 1205 <211> 20 <212> DNA <213> Homo sapiens	
<400> 1205 ggagaccaag gttccagctc	20
<210> 1206 <211> 23 <212> DNA <213> Homo sapiens	
<400> 1206 gaagtcgttg tgaggggttaa agg	23
<210> 1207 <211> 20 <212> DNA <213> Homo sapiens	
<400> 1207 aggtcttcac ctgctctgca	20
<210> 1208 <211> 22 <212> DNA <213> Homo sapiens	
<400> 1208 caaactcaga ttgtgggaga gc	22
<210> 1209 <211> 19 <212> DNA <213> Homo sapiens	
<400> 1209 ttgagttggt tgtcggcaa	19

<210> 1210
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 1210
 gatgctgaat ggggaaaagg 20

<210> 1211
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 1211
 catatactcg ccccatgaag ac 22

<210> 1212
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 1212
 cacaacgaat ggtactacgg c 21

<210> 1213
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 1213
 catcatacat cccctccagc 20

<210> 1214
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 1214
 ctaccacgag caagtctctg 20

<210> 1215
 <211> 24
 <212> DNA
 <213> Homo sapiens

<400> 1215
 ctgktgact caaaccaaat cact 24

<210> 1216
 <211> 27


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<212> DNA
<213> Homo sapiens

<400> 1216
tcaaaaaaatc tcaattcttc cctatct 27

<210> 1217
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1217
catggaaatt cccttcatct g 21

<210> 1218
<211> 18
<212> DNA
<213> Homo sapiens

<400> 1218
cccacgagga ggagccag 18

<210> 1219
<211> 23
<212> DNA
<213> Homo sapiens

<400> 1219
acacacagca tgaagtctgt cac 23

<210> 1220
<211> 18
<212> DNA
<213> Homo sapiens

<400> 1220
cttcctggc cttttctc 18

<210> 1221
<211> 23
<212> DNA
<213> Homo sapiens

<400> 1221
catacaattc tctggttcga tgc 23

<210> 1222
<211> 18
<212> DNA
<213> Homo sapiens

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<400> 1222	
gggagaaaaa gggctgca	18
<210> 1223	
<211> 18	
<212> DNA	
<213> Homo sapiens	
<400> 1223	
cctttcccca cctgctgg	18
<210> 1224	
<211> 18	
<212> DNA	
<213> Homo sapiens	
<400> 1224	
cagcctcagc cgagtggg	18
<210> 1225	
<211> 27	
<212> DNA	
<213> Homo sapiens	
<400> 1225	
gaattgatta tttttgagtg cacagtc	27
<210> 1226	
<211> 24	
<212> DNA	
<213> Homo sapiens	
<400> 1226	
gcaaatttag ccaagtcaaa gaga	24
<210> 1227	
<211> 24	
<212> DNA	
<213> Homo sapiens	
<400> 1227	
gctgaaagac cagaacaaga attc	24
<210> 1228	
<211> 26	
<212> DNA	
<213> Homo sapiens	
<400> 1228	
tggaaaagtt tgtaaccag ataatc	26

<210> 1229
<211> 24
<212> DNA
<213> Homo sapiens

<400> 1229
acatggcaaa gaagtaaatt gctg

24

<210> 1230
<211> 31
<212> DNA
<213> Homo sapiens

<400> 1230
gttaccaaat acaacaacaa taaccagtat t

31

<210> 1231
<211> 27
<212> DNA
<213> Homo sapiens

<400> 1231
tttgaaacca agaatctcct ttaattt

27

<210> 1232
<211> 18
<212> DNA
<213> Homo sapiens

<400> 1232
tgcctccctg ctcatttg

18

<210> 1233
<211> 18
<212> DNA
<213> Homo sapiens

<400> 1233
atgtggcgat tggctctgg

18

<210> 1234
<211> 23
<212> DNA
<213> Homo sapiens

<400> 1234
catggtgtca ttcaggaatt ttg

23

<210> 1235
<211> 28

<212> DNA
 <213> Homo sapiens

<400> 1235
 cagtagaact ggtctttgta ttggtacc 28

<210> 1236
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 1236
 gcagcatcat gggcaccc 18

<210> 1237
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 1237
 gatgcaactc tagcttcttg taaaaatt 28

<210> 1238
 <211> 29
 <212> DNA
 <213> Homo sapiens

<400> 1238
 gatttagcat ataccaatga tctgactct 29

<210> 1239
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 1239
 tttcagatga gttgatttca ttagtgc 27

<210> 1240
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 1240
 cacttgtctt tcagatgagt tgatttc 27

<210> 1241
 <211> 28
 <212> DNA
 <213> Homo sapiens

<400> 1241
ctgtagaggt cagtagaact ggtctttg 28

<210> 1242
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1242
cctcatcgat gtctgcctgc tgtctcc 27

<210> 1243
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1243
gtggtttgca aaccttagca tgcac 25

<210> 1244
<211> 22
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (12)..(12)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1244
tggaagccca gnccccagag gt 22

<210> 1245
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1245
agcccaggcc ccagaggtyc tccca 25

<210> 1246
<211> 27
<212> DNA
<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (14)..(14)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1246
 aatgttgaga angncagcct aaccctg

27

<210> 1247
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (21)..(21)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1247
 cccggsctct tccttcangc ntttcct

27

<210> 1248
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1248
 agaaaagctt gnctcaggca gatcagc

27

<210> 1249
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1249
tacctaaata aataataaaa gccag 25

<210> 1250
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1250
gcaacaagtc tcctttncag aacagtc 27

<210> 1251
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1251
agacttcacc tcttggcanc ttggctt 27

<210> 1252
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1252
ctgcatgttg ctgaagggtg aaaga 25

<210> 1253
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (3)..(3)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (16)..(16)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1253
ttngagcctg tggctncaac cagacct

27

<210> 1254
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (9)..(9)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1254
ttaccctang gctgacctnc caggaac

27

<210> 1255
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1255
tcacctggct cctcaccgag attcc

25

<210> 1256
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (9)..(9)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1256
tatttcagnc cactgacang gcctcag

27

<210> 1257
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1257
accttcataag aggggtataat aaaag

25

<210> 1258
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1258
aagagtttgt ttgaggaaag ggttt

25

<210> 1259
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (18)..(18)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1259
gtaaaggagg tctcnatngc acagggg

27

<210> 1260
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1260
cacagagtag agagnattgc cacgaaa

27

<210> 1261
<211> 25

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<212> DNA
<213> Homo sapiens

<400> 1261
ccagtaattt atgtctttgt gggcc 25

<210> 1262
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1262
atcctgaatt atccaagtgg gccct 25

<210> 1263
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1263
cagcaggaaa caaataacaa gtatc 25

<210> 1264
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (18)..(18)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1264
acaagtatcr ggtaatgncc tctctta 27

<210> 1265
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1265
ctgggacctg ctgnacagag tgctgcc 27

<210> 1266
<211> 27

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<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (9)..(9)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (11)..(11)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1266
tgaaccaana ngcttggcctt tcttatc 27

<210> 1267
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1267
gagccctcct ctgccgtgtc atcaa 25

<210> 1268
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1268
agatctgaac atcacgcct gcac 25

<210> 1269
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1269
cactgggcaa atcngcnggg ctcccc 27

<210> 1270
 <211> 27
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (3)..(3)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (16)..(16)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1270
 gtnggaatga caggtngaag ggagcca

27

<210> 1271
 <211> 27
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (16)..(16)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1271
 ttacaacata acagncatt gagtctt

27

<210> 1272
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1272
 taacagctca ttgagtcttk cacag

25

<210> 1273
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1273
 gggcagtcac tcagcaccag agcac

25

<210> 1274
 <211> 25

<212> DNA
 <213> Homo sapiens

 <400> 1274
 ccctagaaga gtgtgaaaag gaatg 25

 <210> 1275
 <211> 27
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (15)..(15)
 <223> wherein "n" equals a C3 phosphoramidite linker.

 <400> 1275
 attccttcac tcatntatna aacaaaa 27

 <210> 1276
 <211> 25
 <212> DNA
 <213> Homo sapiens

 <400> 1276
 tacgttgagc gatgagcccc aggtt 25

 <210> 1277
 <211> 27
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (16)..(16)
 <223> wherein "n" equals a C3 phosphoramidite linker.

 <220>
 <221> misc_feature
 <222> (19)..(19)
 <223> wherein "n" equals a C3 phosphoramidite linker.

 <400> 1277
 acaggggctg gggatngcna aatacac 27

 <210> 1278
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 1278
gtggtgggca cggagtcctc ac 22

<210> 1279
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1279
gtcagggagg ggcncacctg ggcgcgg 27

<210> 1280
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (7)..(7)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1280
tttttgnagc cttaaaaccc ttccttc 27

<210> 1281
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1281
gcagaagctg tcctgtttcc tgggt 25

<210> 1282
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1282
gaagtgccca ggaggctgnt gacatca 27

<210> 1283
<211> 22
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (13)..(13)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1283
cattgcacca aanctggatg gc

22

<210> 1284
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (7)..(7)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1284
gctttcnggt ggtgncagtg cccagtc

27

<210> 1285
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1285
gagcgaaggg ctggctgagg tcatg

25

<210> 1286
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1286
accttttgct tgatttttca ctgta

25

<210> 1287
<211> 25

<212> DNA
 <213> Homo sapiens
 <400> 1287
 ggctcccaat actgattctg ctcca

25

<210> 1288
 <211> 27
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (18)..(18)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1288
 acccacagca ccctgctnga ccgtctc

27

<210> 1289
 <211> 27
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (16)..(16)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1289
 aggggtgcag ggaganctgg gatgagg

27

<210> 1290
 <211> 27
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (11)..(11)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1290
 gctgggatga ngyctggggt gctgcct

27

<210> 1291
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1291
gttctcttgga gaaaaaactg tgctg 25

<210> 1292
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1292
ccccctctcc aagtctntgt ccacaa 27

<210> 1293
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1293
gaagagggaa ctgaggcagg gacag 25

<210> 1294
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (18)..(18)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1294
aagggtgcta cgtanatntg aggcac 27

<210> 1295
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1295
cccagcgctg gggaaagaaa ggaca 25

<210> 1296
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1296
 gagatgcggg aggaagactg ttaag

25

<210> 1297
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1297
 aagctggaan cctcnaggat ggggttca

27

<210> 1298
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 1298
 aagctctacc acgccttctc ag

22

<210> 1299
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1299
ggaacttgtn ctntcgtgcc cagagca 27

<210> 1300
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1300
tactggcgaa gacagcggcg atggg 25

<210> 1301
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1301
ccagcaggag agccaggacc ca 22

<210> 1302
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1302
ccaagcgcaa ggtgagcagg gg 22

<210> 1303
<211> 22
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (12)..(12)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1303
aggtcggacc ancttttccc aa 22

<210> 1304
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (17)..(17)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (20)..(20)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1304
 tccctatctt tgcnacnctn atgctgt

27

<210> 1305
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (19)..(19)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1305
 acccatactg acccttttng caagtcc

27

<210> 1306
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (21)..(21)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1306
 agagcagttg gaggtcaggt ncagggg

27

<210> 1307
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1307
caaaatcctg cctaatgatg agtgc

25

<210> 1308
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (8)..(8)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1308
tcccttgnac rcaggagtcc ccatccc

27

<210> 1309
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (10)..(10)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1309
gctgtgaagn tcgnggagtt gcccacc

27

<210> 1310
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1310
aaggcrggga tggggactcc tg

22

<210> 1311
<211> 22
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (3)..(3)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1311
tgnggccacc ccagctgtgt ca

22

<210> 1312
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1312
atgtgtgtca cgttctgccca tcacc

25

<210> 1313
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1313
atctggaact tatagtnttg aaaagaa

27

<210> 1314
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1314
gaggggttcc agangtacnt atatttta

27

<210> 1315
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1315
aagtagacaa ggaatgggtg tgaaa

25

<210> 1316
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (11)..(11)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (13)..(13)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1316
tcataatcac nantnaaant tagtagc

27

<210> 1317
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1317
gaaattttgc tgaagagaat gctaa

25

<210> 1318
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1318
cacatgtaaa tgactcagaa taatg

25

<210> 1319
<211> 27

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (16)..(16)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1319
ttcagttcta ggaatnatat cagacac

27

<210> 1320
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (9)..(9)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1320
cttggttaana agcccatna attcttc

27

<210> 1321
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (3)..(3)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1321
ggntggcacc gagntgcag cagccac

27

<210> 1322
<211> 27

<212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (7)..(7)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1322
 aacctcncgc gncatgggct ggaaaca

27

<210> 1323
 <211> 27
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (2)..(2)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1323
 tntcttgac agatgttnat tatgaaa

27

<210> 1324
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1324
 ccggactgnt gtgttctcat caacata

27

<210> 1325
 <211> 27

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (20)..(20)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1325
gatcctggct tggtcantan tctaag

27

<210> 1326
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1326
gaggggaagat tgtggatttg gtcag

25

<210> 1327
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1327
agaccctaaa ataaactctg aggat

25

<210> 1328
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1328
taaaccatat aaagcactcc acaga

25

<210> 1329
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (10)..(10)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (17)..(17)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1329
 tatgaaacgn gtaccanttc tatcccc 27

<210> 1330
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1330
 tgtaaaacga cggccagtag ttctctctcc tccctcact 39

<210> 1331
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1331
 tgtaaaacga cggccagtgg cattcacagg tgattcagt 39

<210> 1332
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1332
 tgtaaaacga cggccagttt ctgggcttta ccctctctc 39

<210> 1333
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1333
 tgtaaaacga cggccagttt ctgggcttta ccctctctc 39

<210> 1334
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1334
 tgtaaaacga cggccagtcc aggtgcagga ttaacagac 39

<210> 1335
 <211> 39

<212> DNA
<213> Homo sapiens

<400> 1335
tgtaaaacga cggccagtac taggaacttg cacagtccg

39

<210> 1336
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1336
tgtaaaacga cggccagtcc tcacacccta tcctacacg

39

<210> 1337
<211> 38
<212> DNA
<213> Homo sapiens

<400> 1337
tgtaaaacga cggccagtca gtgagatctt gccactgc

38

<210> 1338
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1338
tgtaaaacga cggccagtca ggcagacaat gatgtgatg

39

<210> 1339
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1339
tgtaaaacga cggccagtta tccaggtatg gtggcatgt

39

<210> 1340
<211> 37
<212> DNA
<213> Homo sapiens

<400> 1340
tgtaaaacga cggccagtca gaggggaagca cgtgatg

37

<210> 1341
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1341
tgtaaaacga cggccagttg taaagccctt tgcagaagt 39

<210> 1342
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1342
tgtaaaacga cggccagtct ctgaaaagcc ccagagaat 39

<210> 1343
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1343
tgtaaaacga cggccagtga ggctccagac tctcctgtt 39

<210> 1344
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1344
tgtaaaacga cggccagtca ttgcctagaa acctttgca 39

<210> 1345
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1345
tgtaaaacga cggccagtag ccacagctac aatgctgtt 39

<210> 1346
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1346
tgtaaaacga cggccagtct gccgtcaaca cagaactct 39

<210> 1347
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1347
tgtaaaacga cggccagtag aagaacagtt ctcctccgg 39

<210> 1348
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1348
tgtaaaacga cggccagtca tgccttgctt tgtactttc 39

<210> 1349
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1349
tgtaaaacga cggccagtat ggaacacaga ggggttagg 39

<210> 1350
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1350
tgtaaaacga cggccagtgg gttgtatacc acaccctgg 39

<210> 1351
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1351
tgtaaaacga cggccagtcg agataggaaa gccagctag 39

<210> 1352
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1352
tgtaaaacga cggccagtca cttgtggaaa gcacacaga 39

<210> 1353
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1353
tgtaaaacga cggccagtag gaaatttgag gccatcact 39

<210> 1354
<211> 39

<212> DNA
<213> Homo sapiens

<400> 1354
tgtaaaacga cggccagtag cagtcaagat cccttccat 39

<210> 1355
<211> 38
<212> DNA
<213> Homo sapiens

<400> 1355
tgtaaaacga cggccagtga aagagccctc cctctctc 38

<210> 1356
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1356
tgtaaaacga cggccagtca aggtggacag tcttcggta 39

<210> 1357
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1357
tgtaaaacga cggccagttc ctcatagcag ccctattga 39

<210> 1358
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1358
tgtaaaacga cggccagtat ccgaagacag ggagttcat 39

<210> 1359
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1359
tgtaaaacga cggccagtat ccgaagacag ggagttcat 39

<210> 1360
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1360
tgtaaaacga cggccagttc tttgccttcc tggaattct 39

<210> 1361
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1361
tgtaaaacga cggccagtcg tcccagatct gaacatcac 39

<210> 1362
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1362
tgtaaaacga cggccagtga accaagaagc ttggctttc 39

<210> 1363
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1363
tgtaaaacga cggccagtaa cttcccagac tcaagggat 39

<210> 1364
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1364
tgtaaaacga cggccagtca agtgatcctc cactttggt 39

<210> 1365
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1365
tgtaaaacga cggccagtcc tccactttgg tctcccata 39

<210> 1366
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1366
tgtaaaacga cggccagtgc tgtagtctgc cacttcctg 39

<210> 1367
<211> 38
<212> DNA
<213> Homo sapiens

<400> 1367
tgtaaaacga cggccagtag gaccaaggtc tgggaact

38

<210> 1368
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1368
tgtaaaacga cggccagtgc ctggaacaca gaccattaa

39

<210> 1369
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1369
tgtaaaacga cggccagtaa cttcccagac tcaagggat

39

<210> 1370
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1370
tgtaaaacga cggccagtcc cttctgggca gagaatata

39

<210> 1371
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1371
tgtaaaacga cggccagtcc cttctgggca gagaatata

39

<210> 1372
<211> 36
<212> DNA
<213> Homo sapiens

<400> 1372
tgtaaaacga cggccagtgc atcttctctgg tgggtgg

36

<210> 1373
<211> 39

<212> DNA
<213> Homo sapiens

<400> 1373
tgtaaaacga cggccagtcg tcccagatct gaacatcac 39

<210> 1374
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1374
tgtaaaacga cggccagtgt ggtctttaaa ggaggcctg 39

<210> 1375
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1375
tgtaaaacga cggccagtgg tctcagcact gtgatcctc 39

<210> 1376
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1376
tgtaaaacga cggccagttc gggagttgta acaaatgct 39

<210> 1377
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1377
tgtaaaacga cggccagtgc tatgcaaaaa cctcatcca 39

<210> 1378
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1378
tgtaaaacga cggccagtca tctacaccat gcatagggc 39

<210> 1379
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1379
tgtaaaacga cggccagtta gcctctccag ttctagccc 39

<210> 1380
<211> 40
<212> DNA
<213> Homo sapiens

<400> 1380
tgtaaaacga cggccagtaa taaaagagggt gctgaccac 40

<210> 1381
<211> 38
<212> DNA
<213> Homo sapiens

<400> 1381
tgtaaaacga cggccagtcc accatgaccc aagtttat 38

<210> 1382
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1382
tgtaaaacga cggccagtga ggaatccctt tgactcacc 39

<210> 1383
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1383
tgtaaaacga cggccagttg gttccttcaa ctgttgtcc 39

<210> 1384
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1384
tgtaaaacga cggccagtgt ggtcttttaa ggaggcctg 39

<210> 1385
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1385
tgtaaaacga cggccagtag atgtatggcg gaggtttct 39

<210> 1386
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1386
 tgtaaaacga cggccagttt ttggatgtaa acagtgggc 39

<210> 1387
 <211> 39
 <212> DNA
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<400> 1387
 tgtaaaacga cggccagtgg aagcccatg tgaataaat 39

<210> 1388
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1388
 tgtaaaacga cggccagtac ttcagtcgct ccctgggtac 39

<210> 1389
 <211> 39
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<400> 1389
 tgtaaaacga cggccagttc tccatctgaa tgggttctg 39

<210> 1390
 <211> 39
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 <213> Homo sapiens

<400> 1390
 tgtaaaacga cggccagtaa gcaactgtcc ctcaatcct 39

<210> 1391
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 <212> DNA
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<400> 1391
 tgtaaaacga cggccagtga cctccttgct catcagtga 39

<210> 1392
 <211> 39

<212> DNA
<213> Homo sapiens

<400> 1392
tgtaaaacga cggccagtcc ctcacaacga cttcatgtt 39

<210> 1393
<211> 39
<212> DNA
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<400> 1393
tgtaaaacga cggccagttt ctctccaaat gtcctctgtg 39

<210> 1394
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1394
tgtaaaacga cggccagtgg tctcagcact gtgatactc 39

<210> 1395
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1395
tgtaaaacga cggccagtgc aggcaaatac cactttcaa 39

<210> 1396
<211> 39
<212> DNA
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<400> 1396
tgtaaaacga cggccagtcc caatactgat tctgctcca 39

<210> 1397
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1397
tgtaaaacga cggccagttg gttccttcaa ctgttgtcc 39

<210> 1398
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1398
tgtaaaacga cggccagtcc tgactcaatg gacgtttgt 39

<210> 1399
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1399
tgtaaaacga cggccagtcc tgactcaatg gacgtttgt 39

<210> 1400
<211> 39
<212> DNA
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<400> 1400
tgtaaaacga cggccagtat cttcctctgc ctcatcaca 39

<210> 1401
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1401
tgtaaaacga cggccagttc agactttgaa gacatggcc 39

<210> 1402
<211> 39
<212> DNA
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<400> 1402
tgtaaaacga cggccagttg tacgtagcac cctttgctt 39

<210> 1403
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1403
tgtaaaacga cggccagtga atcccaaaga gattgaggc 39

<210> 1404
<211> 39
<212> DNA
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<400> 1404
tgtaaaacga cggccagtga atcccaaaga gattgaggc 39

<210> 1405
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1405
tgtaaaacga cggccagttg cttcctcttt ttcattcaa 39

<210> 1406
<211> 38
<212> DNA
<213> Homo sapiens

<400> 1406
tgtaaaacga cggccagtgg acccacaat caatgctt 38

<210> 1407
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1407
tgtaaaacga cggccagttg ctccacggag ctatttcta 39

<210> 1408
<211> 38
<212> DNA
<213> Homo sapiens

<400> 1408
tgtaaaacga cggccagtgt gggaatgaca ggtggaag 38

<210> 1409
<211> 39
<212> DNA
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<400> 1409
tgtaaaacga cggccagtag agcatcctct cttacccca 39

<210> 1410
<211> 39
<212> DNA
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<400> 1410
tgtaaaacga cggccagtaa gcctggaagc ttaggtctg 39

<210> 1411
<211> 39

<212> DNA
<213> Homo sapiens

<400> 1411
tgtaaaacga cggccagtta ttttctaggt ggggcagct 39

<210> 1412
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<212> DNA
<213> Homo sapiens

<400> 1412
tgtaaaacga cggccagtga accacaggat agagcctcc 39

<210> 1413
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<400> 1413
tgtaaaacga cggccagtac taccagctc ccaacagat 39

<210> 1414
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<400> 1414
tgtaaaacga cggccagtgg acccagatct tcaggtttc 39

<210> 1415
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<400> 1415
tgtaaaacga cggccagtag agtggccaat cttccactt 39

<210> 1416
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<212> DNA
<213> Homo sapiens

<400> 1416
tgtaaaacga cggccagtgg catggggagt catctctac 39

<210> 1417
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<400> 1417
tgtaaaacga cggccagtca gatctgggtt ccaaagaca 39

<210> 1418
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<400> 1418
tgtaaaacga cggccagtct ttgtttcacc ctgtcaagc 39

<210> 1419
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<400> 1419
tgtaaaacga cggccagtgg ctccaggaaa atgagtctt 39

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<212> DNA
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<400> 1420
tgtaaaacga cggccagtaa aagctgggtcc gacctttta 39

<210> 1421
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<400> 1421
tgtaaaacga cggccagttg aggggtgtttc tgatgggtc 39

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<400> 1422
tgtaaaacga cggccagtat ggattttctgg ttccctttg 39

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<400> 1423
tgtaaaacga cggccagtct ttaagagcaa gcgaagtgg 39

<210> 1424
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<400> 1424
tgtaaaacga cggccagtaa ttgtatgtgg gggcagact

39

<210> 1425
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1425
tgtaaaacga cggccagtcc tgacagagcc tgctgatac

39

<210> 1426
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<400> 1426
tgtaaaacga cggccagtgc ccagtttggt catgtcagt

39

<210> 1427
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<400> 1427
tgtaaaacga cggccagtcc tgacagagcc tgctgatac

39

<210> 1428
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tgtaaaacga cggccagtcc ctacccccag taaaatcaa

39

<210> 1429
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<400> 1429
tgtaaaacga cggccagtgc cgtcagagtg ctgtcttat

39

<210> 1430
<211> 40

<212> DNA
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<400> 1430
tgtaaaacga cggccagttg acgagagtca attgaaagga 40

<210> 1431
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<212> DNA
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<400> 1431
tgtaaaacga cggccagtca aagtagttga gcagtggcc 39

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